<110> McCall, Catherine A.
      Tang, Liang
      Heska Corporation

<120> COMPOSITIONS AND METHODS RELATED TO CANINE IgG AND
      CANINE IL-13 RECEPTORS

<130> AL-7

<140> not yet assigned
<141> 2001-04-09

<150> 60/195,659
<151> 2000-04-07

<150> 60/195,874
<151> 2000-04-07

<160> 104

<170> PatentIn Ver. 2.1

<210> 1
<211> 51
<212> DNA
<213> Canis familiaris

<220>
<221> CDS
<222> (1)..(51)

<400> 1
ttc aat gaa tgc aga tgc act gat aca ccc cca tgc cca gtc cct gaa   48
Phe Asn Glu Cys Arg Cys Thr Asp Thr Pro Pro Cys Pro Val Pro Glu
  1   5   10   15

cct   51
Pro

<210> 2
<211> 17
<212> PRT
<213> Canis familiaris

<400> 2

```
Phe Asn Glu Cys Arg Cys Thr Asp Thr Pro Pro Cys Pro Val Pro Glu
 1               5                   10                  15

Pro
```

```
<210> 3
<211> 51
<212> DNA
<213> Canis familiaris

<400> 3
aggttcaggg actgggcatg ggggtgtatc agtgcatctg cattcattga a          51
```

```
<210> 4
<211> 1654
<212> DNA
<213> Canis familiaris

<220>
<221> CDS
<222> (70)..(1473)

<400> 4
ggcacgagcc agcccccagg atccccaggt gaccccattc agtgctcagg acacaacaca 60

gacaccacc atg gag tct gtg ttc tgc tgg gtt ttc ctt gtc gtt att tta 111
          Met Glu Ser Val Phe Cys Trp Val Phe Leu Val Val Ile Leu
           1               5                   10

aaa ggt gtc cag ggt gag gtg cag ttg gtg gag tct ggg gga gac ctg   159
Lys Gly Val Gln Gly Glu Val Gln Leu Val Glu Ser Gly Gly Asp Leu
 15              20                  25                  30

gtg aag cct ggg ggg tcc ctg aga ctc tcc tgt gtg gcc tct gga ttc   207
Val Lys Pro Gly Gly Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe
                35                  40                  45

acc ttc agt tcg tac tac atg cat tgg atc cgc cag gct cca ggg aag   255
Thr Phe Ser Ser Tyr Tyr Met His Trp Ile Arg Gln Ala Pro Gly Lys
            50                  55                  60

ggg ctt cag cgg gtc gca cat att aga ggt gat gga agg act aca cac   303
Gly Leu Gln Arg Val Ala His Ile Arg Gly Asp Gly Arg Thr Thr His
            65                  70                  75
```

2

```
tac gca gac gct atg aag ggc cga ttc acc atc tcc aga gac aac gcc      351
Tyr Ala Asp Ala Met Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala
     80                  85                  90

aag aac acg ctg tat ctg cag atg aat agc ctg aca gtc gaa gac acg      399
Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Thr Val Glu Asp Thr
 95                 100                 105                 110

gct att tat tac tgt gta aag gac ata tac tat ggg gtc ggg gac tat      447
Ala Ile Tyr Tyr Cys Val Lys Asp Ile Tyr Tyr Gly Val Gly Asp Tyr
                115                 120                 125

tgg ggc cag gga acc ctg gtc acc gtc tcc tca gcc tcc acc acg gcc      495
Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Thr Ala
             130                 135                 140

ccc tcg gtt ttc cca ctg gcc ccc agc tgc ggg tcc act tcc ggc tcc      543
Pro Ser Val Phe Pro Leu Ala Pro Ser Cys Gly Ser Thr Ser Gly Ser
         145                 150                 155

acg gtg gcc ctg gcc tgc ctg gtg tca ggc tac ttc ccc gag cct gta      591
Thr Val Ala Leu Ala Cys Leu Val Ser Gly Tyr Phe Pro Glu Pro Val
     160                 165                 170

act gtg tcc tgg aat tcc ggc tcc ttg acc agc ggt gtg cac acc ttc      639
Thr Val Ser Trp Asn Ser Gly Ser Leu Thr Ser Gly Val His Thr Phe
175                 180                 185                 190

ccg tcc gtc ctg cag tcc tca ggg ctt cac tcc ctc agc agc atg gtg      687
Pro Ser Val Leu Gln Ser Ser Gly Leu His Ser Leu Ser Ser Met Val
             195                 200                 205

aca gtg ccc tcc agc agg tgg ccc agc gag acc ttc acc tgc aac gtg      735
Thr Val Pro Ser Ser Arg Trp Pro Ser Glu Thr Phe Thr Cys Asn Val
             210                 215                 220

gtc cac cca gcc agc aac act aaa gta gac aag cca gtg ttc aat gaa      783
Val His Pro Ala Ser Asn Thr Lys Val Asp Lys Pro Val Phe Asn Glu
         225                 230                 235

tgc aga tgc act gat aca ccc cca tgc cca gtc cct gaa cct ctg gga      831
Cys Arg Cys Thr Asp Thr Pro Pro Cys Pro Val Pro Glu Pro Leu Gly
     240                 245                 250

ggg cct tcg gtc ctc atc ttt ccc ccg aaa ccc aag gac atc ctc agg      879
Gly Pro Ser Val Leu Ile Phe Pro Pro Lys Pro Lys Asp Ile Leu Arg
255                 260                 265                 270
```

3

```
att acc cga aca ccc gag gtc acc tgt gtg gtg tta gat ctg ggc cgt      927
Ile Thr Arg Thr Pro Glu Val Thr Cys Val Val Leu Asp Leu Gly Arg
            275                 280                 285

gag gac cct gag gtg cag atc agc tgg ttc gtg gat ggt aag gag gtg      975
Glu Asp Pro Glu Val Gln Ile Ser Trp Phe Val Asp Gly Lys Glu Val
            290                 295                 300

cac aca gcc aag acc cag tct cgt gag cag cag ttc aac ggc acc tac     1023
His Thr Ala Lys Thr Gln Ser Arg Glu Gln Gln Phe Asn Gly Thr Tyr
            305                 310                 315

cgt gtg gtc agc gtc ctc ccc att gag cac cag gac tgg ctc aca ggg     1071
Arg Val Val Ser Val Leu Pro Ile Glu His Gln Asp Trp Leu Thr Gly
            320                 325                 330

aag gag ttc aag tgc aga gtc aac cac ata gac ctc ccg tct ccc atc     1119
Lys Glu Phe Lys Cys Arg Val Asn His Ile Asp Leu Pro Ser Pro Ile
335                 340                 345                 350

gag agg acc atc tct aag gcc aga ggg agg gcc cat aag ccc agt gtg     1167
Glu Arg Thr Ile Ser Lys Ala Arg Gly Arg Ala His Lys Pro Ser Val
            355                 360                 365

tat gtc ctg ccg cca tcc cca aag gag ttg tca tcc agt gac aca gtc     1215
Tyr Val Leu Pro Pro Ser Pro Lys Glu Leu Ser Ser Ser Asp Thr Val
            370                 375                 380

agc atc acc tgc ctg ata aaa gac ttc tac cca cct gac att gat gtg     1263
Ser Ile Thr Cys Leu Ile Lys Asp Phe Tyr Pro Pro Asp Ile Asp Val
            385                 390                 395

gag tgg cag agc aat gga cag cag gag ccc gag agg aag cac cgc atg     1311
Glu Trp Gln Ser Asn Gly Gln Gln Glu Pro Glu Arg Lys His Arg Met
            400                 405                 410

acc ccg ccc cag ctg gac gag gac ggg tcc tac ttc ctg tac agc aag     1359
Thr Pro Pro Gln Leu Asp Glu Asp Gly Ser Tyr Phe Leu Tyr Ser Lys
415                 420                 425                 430

ctc tct gtg gac aag agc cgc tgg cag cag gga gac ccc ttc aca tgt     1407
Leu Ser Val Asp Lys Ser Arg Trp Gln Gln Gly Asp Pro Phe Thr Cys
            435                 440                 445

gcg gtg atg cat gaa act cta cag aac cac tac aca gat cta tcc ctc     1455
Ala Val Met His Glu Thr Leu Gln Asn His Tyr Thr Asp Leu Ser Leu
            450                 455                 460
```

4

```
tcc cat tct ccg ggt aaa tgagcaacac gcccggcacc cagcaagccc          1503
Ser His Ser Pro Gly Lys
            465


cccacccttg gctctcagga tcccctgagg acacctgagc ccctgtccct gtgtacataa 1563

ccctgggtag gcacccatca tgaaataaag cacccagcac tgccctgggc cctgcaaaaa 1623

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa a                                1654



<210> 5
<211> 468
<212> PRT
<213> Canis familiaris

<400> 5
Met Glu Ser Val Phe Cys Trp Val Phe Leu Val Val Ile Leu Lys Gly
 1               5                  10                  15

Val Gln Gly Glu Val Gln Leu Val Glu Ser Gly Gly Asp Leu Val Lys
            20                  25                  30

Pro Gly Gly Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Phe
        35                  40                  45

Ser Ser Tyr Tyr Met His Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu
    50                  55                  60

Gln Arg Val Ala His Ile Arg Gly Asp Gly Arg Thr Thr His Tyr Ala
 65                  70                  75                  80

Asp Ala Met Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn
                85                  90                  95

Thr Leu Tyr Leu Gln Met Asn Ser Leu Thr Val Glu Asp Thr Ala Ile
            100                 105                 110

Tyr Tyr Cys Val Lys Asp Ile Tyr Tyr Gly Val Gly Asp Tyr Trp Gly
            115                 120                 125

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Thr Ala Pro Ser
        130                 135                 140

Val Phe Pro Leu Ala Pro Ser Cys Gly Ser Thr Ser Gly Ser Thr Val
145                 150                 155                 160
```

5

Ala Leu Ala Cys Leu Val Ser Gly Tyr Phe Pro Glu Pro Val Thr Val
           165   170   175

Ser Trp Asn Ser Gly Ser Leu Thr Ser Gly Val His Thr Phe Pro Ser
          180   185   190

Val Leu Gln Ser Ser Gly Leu His Ser Leu Ser Ser Met Val Thr Val
          195   200   205

Pro Ser Ser Arg Trp Pro Ser Glu Thr Phe Thr Cys Asn Val Val His
          210   215   220

Pro Ala Ser Asn Thr Lys Val Asp Lys Pro Val Phe Asn Glu Cys Arg
225   230   235   240

Cys Thr Asp Thr Pro Pro Cys Pro Val Pro Glu Pro Leu Gly Gly Pro
                245   250   255

Ser Val Leu Ile Phe Pro Pro Lys Pro Lys Asp Ile Leu Arg Ile Thr
          260   265   270

Arg Thr Pro Glu Val Thr Cys Val Val Leu Asp Leu Gly Arg Glu Asp
          275   280   285

Pro Glu Val Gln Ile Ser Trp Phe Val Asp Gly Lys Glu Val His Thr
          290   295   300

Ala Lys Thr Gln Ser Arg Glu Gln Gln Phe Asn Gly Thr Tyr Arg Val
305   310   315   320

Val Ser Val Leu Pro Ile Glu His Gln Asp Trp Leu Thr Gly Lys Glu
          325   330   335

Phe Lys Cys Arg Val Asn His Ile Asp Leu Pro Ser Pro Ile Glu Arg
          340   345   350

Thr Ile Ser Lys Ala Arg Gly Arg Ala His Lys Pro Ser Val Tyr Val
          355   360   365

Leu Pro Pro Ser Pro Lys Glu Leu Ser Ser Ser Asp Thr Val Ser Ile
          370   375   380

Thr Cys Leu Ile Lys Asp Phe Tyr Pro Pro Asp Ile Asp Val Glu Trp
385   390   395   400

Gln Ser Asn Gly Gln Gln Glu Pro Glu Arg Lys His Arg Met Thr Pro
          405   410   415

Pro Gln Leu Asp Glu Asp Gly Ser Tyr Phe Leu Tyr Ser Lys Leu Ser
        420   425   430

Val Asp Lys Ser Arg Trp Gln Gln Gly Asp Pro Phe Thr Cys Ala Val
        435   440   445

Met His Glu Thr Leu Gln Asn His Tyr Thr Asp Leu Ser Leu Ser His
    450   455   460

Ser Pro Gly Lys
465

<210> 6
<211> 1654
<212> DNA
<213> Canis familiaris

<400> 6
tttttttttt tttttttttt tttttttttt tttttgcag ggcccagggc agtgctgggt 60
gctttatttc atgatgggtg cctacccagg gttatgtaca cagggacagg ggctcaggtg 120
tcctcagggg atcctgagag ccaagggtgg ggggcttgct gggtgccggg cgtgttgctc 180
atttacccgg agaatgggag agggatagat ctgtgtagtg gttctgtaga gtttcatgca 240
tcaccgcaca tgtgaagggg tctccctgct gccagcggct cttgtccaca gagagcttgc 300
tgtacaggaa gtaggacccg tcctcgtcca gctggggcgg ggtcatgcgg tgcttcctct 360
cgggctcctg ctgtccattg ctctgccact ccacatcaat gtcaggtggg tagaagtctt 420
ttatcaggca ggtgatgctg actgtgtcac tggatgacaa ctcctttggg gatggcggca 480
ggacatacac actgggctta tgggccctcc ctctggcctt agagatggtc ctctcgatgg 540
gagacgggag gtctatgtgg ttgactctgc acttgaactc cttccctgtg agccagtcct 600
ggtgctcaat ggggaggacg ctgaccacac ggtaggtgcc gttgaactgc tgctcacgag 660
actgggtctt ggctgtgtgc acctccttac catccacgaa ccagctgatc tgcacctcag 720
ggtcctcacg gcccagatct aacaccacac aggtgacctc gggtgttcgg gtaatcctga 780
ggatgtcctt gggtttcggg ggaaagatga ggaccgaagg ccctcccaga ggttcaggga 840
ctgggcatgg gggtgtatca gtgcatctgc attcattgaa cactggcttg tctactttag 900
tgttgctggc tgggtggacc acgttgcagg tgaaggtctc gctgggccac ctgctggagg 960
gcactgtcac catgctgctg agggagtgaa gccctgagga ctgcaggacg gacgggaagg 1020
tgtgcacacc gctggtcaag gagccggaat tccaggacac agttacaggc tcggggaagt 1080
agcctgacac caggcaggcc agggccaccg tggagccgga agtggacccg cagctggggg 1140
ccagtgggaa aaccgagggg gccgtggtgg aggctgagga gacggtgacc agggttccct 1200
ggccccaata gtccccgacc ccatagtata tgtcctttac acagtaataa atagccgtgt 1260
cttcgactgt caggctattc atctgcagat acagcgtgtt cttggcgttg tctctggaga 1320
tggtgaatcg gcccttcata gcgtctgcgt agtgtgtagt ccttccatca cctctaatat 1380
gtgcgacccg ctgaagcccc ttccctggag cctggcggat ccaatgcatg tagtacgaac 1440
tgaaggtgaa tccagaggcc acacaggaga gtctcaggga ccccccaggc ttcaccaggt 1500
ctcccccaga ctccaccaac tgcacctcac cctggacacc ttttaaaata acgacaagga 1560
aaacccagca gaacacagac tccatggtgg tgtctgtgtt gtgtcctgag cactgaatgg 1620
ggtcacctgg ggatcctggg ggctggctcg tgcc   1654

7

<210> 7
<211> 51
<212> DNA
<213> Canis familiaris

<220>
<221> CDS
<222> (1)..(51)

<400> 7
ccc aaa gag tcc acc tgc aag tgt ata tcc cca tgc cca gtc cct gaa   48
Pro Lys Glu Ser Thr Cys Lys Cys Ile Ser Pro Cys Pro Val Pro Glu
 1   5   10   15

tca   51
Ser

<210> 8
<211> 17
<212> PRT
<213> Canis familiaris

<400> 8
Pro Lys Glu Ser Thr Cys Lys Cys Ile Ser Pro Cys Pro Val Pro Glu
 1   5   10   15

Ser

<210> 9
<211> 51
<212> DNA
<213> Canis familiaris

<400> 9
tgattcaggg actgggcatg gggatataca cttgcaggtg gactctttgg g   51

<210> 10
<211> 1460
<212> DNA
<213> Canis familiaris

<220>
<221> CDS
<222> (48)..(1457)

<400> 10
ccaggtgacc ccattcagtg ctcaggacac aacacagaca aaccacc atg gag tct   56
                                                     Met Glu Ser
                                                       1

gtg ctc tgc tgg gtt ttc ctt gtc tct att tta aaa ggt gtc cag ggt   104
Val Leu Cys Trp Val Phe Leu Val Ser Ile Leu Lys Gly Val Gln Gly
          5   10   15

gag gtg caa ctg gtg gag tct ggg gga gac ctg gtg aag cct ggg ggg   152
Glu Val Gln Leu Val Glu Ser Gly Gly Asp Leu Val Lys Pro Gly Gly
 20   25   30   35

tcc ttg aga ctg tcc tgt gtg gcc tct gga ttc acc ttc agt gac tat   200
Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Phe Ser Asp Tyr
                 40   45   50

ggc atg agt tgg gtc cgt cag tct cca ggg aag ggg ctg cag tgg gtc   248
Gly Met Ser Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Gln Trp Val
             55   60   65

gca gct gtt agc aat cgt gga gat act tac tac gca gac gct gtg aag   296
Ala Ala Val Ser Asn Arg Gly Asp Thr Tyr Tyr Ala Asp Ala Val Lys
         70   75   80

ggc cga ttc acc atc tcc aga gac aac gcc aag aac acg ctg tat ctc   344
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr Leu
     85   90   95

cag atg agc agc ctg aaa gcc gag gac acg gca atc tat cac tgt gtg   392
Gln Met Ser Ser Leu Lys Ala Glu Asp Thr Ala Ile Tyr His Cys Val
100   105   110   115

acg gga gta tgg ccg cga cat tat tat ggt atg gac cac tgg ggc aat   440
Thr Gly Val Trp Pro Arg His Tyr Tyr Gly Met Asp His Trp Gly Asn
                 120   125   130

ggc acc tca ctc ttc gtg tcc tca gcc tcc acc acg gcc ccc tcg gtt   488
Gly Thr Ser Leu Phe Val Ser Ser Ala Ser Thr Thr Ala Pro Ser Val
             135   140   145

ttc cca ctg gcc ccc agc tgc ggg tcc act tcc ggc tcc acg gtg gcc   536
Phe Pro Leu Ala Pro Ser Cys Gly Ser Thr Ser Gly Ser Thr Val Ala
         150   155   160

9

```
ctg gcc tgc ctg gtg tca ggc tac ttc ccc gag cct gta act gtg tcc    584
Leu Ala Cys Leu Val Ser Gly Tyr Phe Pro Glu Pro Val Thr Val Ser
    165             170             175

tgg aat tcc ggc tcc ttg acc agc ggt gtg cac acc ttc ccg tcc gtc    632
Trp Asn Ser Gly Ser Leu Thr Ser Gly Val His Thr Phe Pro Ser Val
180             185             190             195

ctg cag tcc tca ggg ctc tac tcc ctc agc agc acg gtg aca gtg ccc    680
Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Thr Val Thr Val Pro
            200             205             210

tcc agc agg tgg ccc agc gag acc ttc acc tgc aac gtg gtc cac ccg    728
Ser Ser Arg Trp Pro Ser Glu Thr Phe Thr Cys Asn Val Val His Pro
            215             220             225

gcc agc aac act aaa gta gac aag cca gtg ccc aaa gag tcc acc tgc    776
Ala Ser Asn Thr Lys Val Asp Lys Pro Val Pro Lys Glu Ser Thr Cys
            230             235             240

aag tgt ata tcc cca tgc cca gtc cct gaa tca ctg gga ggg cct tcg    824
Lys Cys Ile Ser Pro Cys Pro Val Pro Glu Ser Leu Gly Gly Pro Ser
    245             250             255

gtc ttc atc ttt ccc ccg aaa ccc aag gac atc ctc agg att acc cga    872
Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Ile Leu Arg Ile Thr Arg
260             265             270             275

aca ccc gag atc acc tgt gtg gtg tta gat ctg ggc cgt gag gac cct    920
Thr Pro Glu Ile Thr Cys Val Val Leu Asp Leu Gly Arg Glu Asp Pro
            280             285             290

gag gtg cag atc agc tgg ttc gtg gat ggt aag gag gtg cac aca gcc    968
Glu Val Gln Ile Ser Trp Phe Val Asp Gly Lys Glu Val His Thr Ala
            295             300             305

aag acg cag cct cgt gag cag cag ttc aac agc acc tac cgt gtg gtc    1016
Lys Thr Gln Pro Arg Glu Gln Gln Phe Asn Ser Thr Tyr Arg Val Val
            310             315             320

agc gtc ctc ccc att gag cac cag gac tgg ctc acc gga aag gag ttc    1064
Ser Val Leu Pro Ile Glu His Gln Asp Trp Leu Thr Gly Lys Glu Phe
    325             330             335

aag tgc aga gtc aac cac ata ggc ctc ccg tcc ccc atc gag agg act    1112
Lys Cys Arg Val Asn His Ile Gly Leu Pro Ser Pro Ile Glu Arg Thr
340             345             350             355
```

10

```
atc tcc aaa gcc aga ggg caa gcc cat cag ccc agt gtg tat gtc ctg    1160
Ile Ser Lys Ala Arg Gly Gln Ala His Gln Pro Ser Val Tyr Val Leu
            360                 365                 370

cca cca tcc cca aag gag ttg tca tcc agt gac acg gtc acc ctg acc    1208
Pro Pro Ser Pro Lys Glu Leu Ser Ser Ser Asp Thr Val Thr Leu Thr
            375                 380                 385

tgc ctg atc aaa gac ttc ttc cca cct gag att gat gtg gag tgg cag    1256
Cys Leu Ile Lys Asp Phe Phe Pro Pro Glu Ile Asp Val Glu Trp Gln
            390                 395                 400

agc aat gga cag ccg gag ccc gag agc aag tac cac acg act gcg ccc    1304
Ser Asn Gly Gln Pro Glu Pro Glu Ser Lys Tyr His Thr Thr Ala Pro
            405                 410                 415

cag ctg gac gag gac ggg tcc tac ttc ctg tac agc aag ctc tct gtg    1352
Gln Leu Asp Glu Asp Gly Ser Tyr Phe Leu Tyr Ser Lys Leu Ser Val
420                 425                 430                 435

gac aag agc cgc tgg cag cag gga gac acc ttc aca tgt gcg gtg atg    1400
Asp Lys Ser Arg Trp Gln Gln Gly Asp Thr Phe Thr Cys Ala Val Met
            440                 445                 450

cat gaa gct cta cag aac cac tac aca gat cta tcc ctc tcc cat tct    1448
His Glu Ala Leu Gln Asn His Tyr Thr Asp Leu Ser Leu Ser His Ser
            455                 460                 465

ccg ggt aaa tga                                                     1460
Pro Gly Lys
            470


<210> 11
<211> 470
<212> PRT
<213> Canis familiaris

<400> 11
Met Glu Ser Val Leu Cys Trp Val Phe Leu Val Ser Ile Leu Lys Gly
  1               5                  10                  15

Val Gln Gly Glu Val Gln Leu Val Glu Ser Gly Gly Asp Leu Val Lys
            20                  25                  30

Pro Gly Gly Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Phe
            35                  40                  45
```

11

Ser Asp Tyr Gly Met Ser Trp Val Arg Gln Ser Pro Gly Lys Gly Leu
         50   55   60

Gln Trp Val Ala Ala Val Ser Asn Arg Gly Asp Thr Tyr Tyr Ala Asp
65   70   75   80

Ala Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr
                   85   90   95

Leu Tyr Leu Gln Met Ser Ser Leu Lys Ala Glu Asp Thr Ala Ile Tyr
              100   105   110

His Cys Val Thr Gly Val Trp Pro Arg His Tyr Tyr Gly Met Asp His
         115   120   125

Trp Gly Asn Gly Thr Ser Leu Phe Val Ser Ser Ala Ser Thr Thr Ala
      130   135   140

Pro Ser Val Phe Pro Leu Ala Pro Ser Cys Gly Ser Thr Ser Gly Ser
145   150   155   160

Thr Val Ala Leu Ala Cys Leu Val Ser Gly Tyr Phe Pro Glu Pro Val
                   165   170   175

Thr Val Ser Trp Asn Ser Gly Ser Leu Thr Ser Gly Val His Thr Phe
              180   185   190

Pro Ser Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Thr Val
         195   200   205

Thr Val Pro Ser Ser Arg Trp Pro Ser Glu Thr Phe Thr Cys Asn Val
      210   215   220

Val His Pro Ala Ser Asn Thr Lys Val Asp Lys Pro Val Pro Lys Glu
225   230   235   240

Ser Thr Cys Lys Cys Ile Ser Pro Cys Pro Val Pro Glu Ser Leu Gly
                   245   250   255

Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Ile Leu Arg
              260   265   270

Ile Thr Arg Thr Pro Glu Ile Thr Cys Val Val Leu Asp Leu Gly Arg
         275   280   285

Glu Asp Pro Glu Val Gln Ile Ser Trp Phe Val Asp Gly Lys Glu Val
      290   295   300

His Thr Ala Lys Thr Gln Pro Arg Glu Gln Gln Phe Asn Ser Thr Tyr
305   310   315   320

Arg Val Val Ser Val Leu Pro Ile Glu His Gln Asp Trp Leu Thr Gly
            325   330   335

Lys Glu Phe Lys Cys Arg Val Asn His Ile Gly Leu Pro Ser Pro Ile
        340   345   350

Glu Arg Thr Ile Ser Lys Ala Arg Gly Gln Ala His Gln Pro Ser Val
        355   360   365

Tyr Val Leu Pro Pro Ser Pro Lys Glu Leu Ser Ser Ser Asp Thr Val
    370   375   380

Thr Leu Thr Cys Leu Ile Lys Asp Phe Phe Pro Pro Glu Ile Asp Val
385   390   395   400

Glu Trp Gln Ser Asn Gly Gln Pro Glu Pro Glu Ser Lys Tyr His Thr
            405   410   415

Thr Ala Pro Gln Leu Asp Glu Asp Gly Ser Tyr Phe Leu Tyr Ser Lys
        420   425   430

Leu Ser Val Asp Lys Ser Arg Trp Gln Gln Gly Asp Thr Phe Thr Cys
        435   440   445

Ala Val Met His Glu Ala Leu Gln Asn His Tyr Thr Asp Leu Ser Leu
    450   455   460

Ser His Ser Pro Gly Lys
465   470

<210> 12
<211> 1460
<212> DNA
<213> Canis familiaris

<400> 12
tcatttaccc ggagaatggg agagggatag atctgtgtag tggttctgta gagcttcatg 60
catcaccgca catgtgaagg tgtctccctg ctgccagcgg ctcttgtcca cagagagctt 120
gctgtacagg aagtaggacc cgtcctcgtc cagctggggc gcagtcgtgt ggtacttgct 180
ctcgggctcc ggctgtccat tgctctgcca ctccacatca atctcaggtg ggaagaagtc 240
tttgatcagg caggtcaggg tgaccgtgtc actggatgac aactcctttg gggatggtgg 300
caggacatac acactgggct gatgggcttg ccctctggct ttggagatag tcctctcgat 360

13

```
gggggacggg aggcctatgt ggttgactct gcacttgaac tcctttccgg tgagccagtc  420
ctggtgctca atggggagga cgctgaccac acggtaggtg ctgttgaact gctgctcacg  480
aggctgcgtc ttggctgtgt gcacctcctt accatccacg aaccagctga tctgcacctc  540
agggtcctca cggcccagat ctaacaccac acaggtgatc tcgggtgttc gggtaatcct  600
gaggatgtcc ttgggtttcg ggggaaagat gaagaccgaa ggccctccca gtgattcagg  660
gactgggcat ggggatatac acttgcaggt ggactctttg ggcactggct tgtctacttt  720
agtgttgctg gccgggtgga ccacgttgca ggtgaaggtc tcgctgggcc acctgctgga  780
gggcactgtc accgtgctgc tgagggagta gagccctgag gactgcagga cggacgggaa  840
ggtgtgcaca ccgctggtca aggagccgga attccaggac acagttacag gctcggggaa  900
gtagcctgac accaggcagg ccagggccac cgtggagccg gaagtggacc cgcagctggg  960
ggccagtggg aaaaccgagg gggccgtggt ggaggctgag gacacgaaga gtgaggtgcc 1020
attgccccag tggtccatac cataataatg tcgcggccat actcccgtca cacagtgata 1080
gattgccgtg tcctcggctt tcaggctgct catctggaga tacagcgtgt tcttggcgtt 1140
gtctctggag atggtgaatc ggcccttcac agcgtctgcg tagtaagtat ctccacgatt 1200
gctaacagct gcgacccact gcagcccctt ccctggagac tgacggaccc aactcatgcc 1260
atagtcactg aaggtgaatc cagaggccac acaggacagt ctcaaggacc ccccaggctt 1320
caccaggtct cccccagact ccaccagttg cacctcaccc tggacacctt ttaaaataga 1380
gacaaggaaa acccagcaga gcacagactc catggtggtt tgtctgtgtt gtgtcctgag 1440
cactgaatgg ggtcacctgg                                             1460


<210> 13
<211> 60
<212> DNA
<213> Canis familiaris

<220>
<221> CDS
<222> (1)..(60)

<400> 13
gcc aaa gaa tgc gag tgc aag tgt aac tgt aac aac tgc cca tgc cca    48
Ala Lys Glu Cys Glu Cys Lys Cys Asn Cys Asn Asn Cys Pro Cys Pro
  1               5                  10                  15

ggt tgt ggc ctg                                                     60
Gly Cys Gly Leu
            20



<210> 14
<211> 20
<212> PRT
<213> Canis familiaris

<400> 14
Ala Lys Glu Cys Glu Cys Lys Cys Asn Cys Asn Asn Cys Pro Cys Pro
  1               5                  10                  15
```

14

Gly Cys Gly Leu
        20

<210> 15
<211> 60
<212> DNA
<213> Canis familiaris

<400> 15
caggccacaa cctgggcatg ggcagttgtt acagttacac ttgcactcgc attctttggc 60

<210> 16
<211> 1456
<212> DNA
<213> Canis familiaris

<220>
<221> CDS
<222> (32)..(1453)

<220>
<223> At location 27, n = unknown

<400> 16
aagtgctcag gcacaacaca gacaaancac c atg gag tct gtg ctc tac tgg   52
                                       Met Glu Ser Val Leu Tyr Trp
                                       1   5

gtt ttc ctt gtc gct att tta aag ggt gtc cag ggt gac gtg cag ctg   100
Val Phe Leu Val Ala Ile Leu Lys Gly Val Gln Gly Asp Val Gln Leu
        10   15   20

gtg gag tct ggg gga gac ctg gtg aag cct ggg ggg tcc ttg aga ctg   148
Val Glu Ser Gly Gly Asp Leu Val Lys Pro Gly Gly Ser Leu Arg Leu
     25   30   35

tcc tgt gtg gcc tct gga ttc acc ttt agt agc tgt gcc atg agc tgg   196
Ser Cys Val Ala Ser Gly Phe Thr Phe Ser Ser Cys Ala Met Ser Trp
 40   45   50   55

gtc cgt cag tct cca ggg aag ggg cct cag tgg gtc gca act att cgg   244
Val Arg Gln Ser Pro Gly Lys Gly Pro Gln Trp Val Ala Thr Ile Arg
               60   65   70

15

```
tat gat gga agt gat ata tac tac gca gac gct gtg aag ggc cga ttc    292
Tyr Asp Gly Ser Asp Ile Tyr Tyr Ala Asp Ala Val Lys Gly Arg Phe
                75                  80                  85

agc atc tcc aga gac aac gcc aag aac acg gtg tat ctg cag atg aac    340
Ser Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Tyr Leu Gln Met Asn
                90                  95                 100

agc ctg aga gcc gag gac acg gcc gtg tat tat tgt gcg aag gcc ccc    388
Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Lys Ala Pro
        105                 110                 115

ccc tac gat agt tac cac tat ggt atg gac tat tgg ggt cct ggc act    436
Pro Tyr Asp Ser Tyr His Tyr Gly Met Asp Tyr Trp Gly Pro Gly Thr
120                 125                 130                 135

tcc ctc ttc gtg tcg tca gcc tcc acc acg gcc ccc tcg gtt ttc cca    484
Ser Leu Phe Val Ser Ser Ala Ser Thr Thr Ala Pro Ser Val Phe Pro
                140                 145                 150

ctg gcc ccc agc tgt ggg tcc caa tcc ggc tcc acg gtg gcc ctg gcc    532
Leu Ala Pro Ser Cys Gly Ser Gln Ser Gly Ser Thr Val Ala Leu Ala
                155                 160                 165

tgc ctg gtg tca ggc tac atc ccc gag cct gta act gtg tcc tgg aat    580
Cys Leu Val Ser Gly Tyr Ile Pro Glu Pro Val Thr Val Ser Trp Asn
                170                 175                 180

tcc gtc tcc ttg acc agc ggt gtg cac acc ttc ccg tcc gtc ctg cag    628
Ser Val Ser Leu Thr Ser Gly Val His Thr Phe Pro Ser Val Leu Gln
        185                 190                 195

tcc tca ggg ctc tac tcc ctc agc agc atg gtg aca gtg ccc tcc agc    676
Ser Ser Gly Leu Tyr Ser Leu Ser Ser Met Val Thr Val Pro Ser Ser
200                 205                 210                 215

agg tgg ccc agc gag acc ttc acc tgc aat gtg gcc cac ccg gcc acc    724
Arg Trp Pro Ser Glu Thr Phe Thr Cys Asn Val Ala His Pro Ala Thr
                220                 225                 230

aac act aaa gta gac aag cca gtg gcc aaa gaa tgc gag tgc aag tgt    772
Asn Thr Lys Val Asp Lys Pro Val Ala Lys Glu Cys Glu Cys Lys Cys
                235                 240                 245

aac tgt aac aac tgc cca tgc cca ggt tgt ggc ctg ctg gga ggg cct    820
Asn Cys Asn Asn Cys Pro Cys Pro Gly Cys Gly Leu Leu Gly Gly Pro
        250                 255                 260
```

16

```
tcg gtc ttc atc ttt ccc cca aaa ccc aag gac atc ctc gtg act gcc      868
Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Ile Leu Val Thr Ala
    265                 270                 275

cgg aca ccc aca gtc act tgt gtg gtg gtg gat ctg gac cca gaa aac      916
Arg Thr Pro Thr Val Thr Cys Val Val Val Asp Leu Asp Pro Glu Asn
280                 285                 290                 295

cct gag gtg cag atc agc tgg ttc gtg gat agt aag cag gtg caa aca      964
Pro Glu Val Gln Ile Ser Trp Phe Val Asp Ser Lys Gln Val Gln Thr
                300                 305                 310

gcc aac acg cag cct cgt gag gag cag tcc aat ggc acc tac cgt gtg     1012
Ala Asn Thr Gln Pro Arg Glu Glu Gln Ser Asn Gly Thr Tyr Arg Val
                315                 320                 325

gtc agt gtc ctc ccc att ggg cac cag gac tgg ctt tca ggg aag cag     1060
Val Ser Val Leu Pro Ile Gly His Gln Asp Trp Leu Ser Gly Lys Gln
            330                 335                 340

ttc aag tgc aaa gtc aac aac aaa gcc ctc cca tcc ccc att gag gag     1108
Phe Lys Cys Lys Val Asn Asn Lys Ala Leu Pro Ser Pro Ile Glu Glu
        345                 350                 355

atc atc tcc aag acc cca ggg cag gcc cat cag cct aat gtg tat gtc     1156
Ile Ile Ser Lys Thr Pro Gly Gln Ala His Gln Pro Asn Val Tyr Val
360                 365                 370                 375

ctg ccg cca tcg cgg gat gag atg agc aag aat acg gtc acc ctg acc     1204
Leu Pro Pro Ser Arg Asp Glu Met Ser Lys Asn Thr Val Thr Leu Thr
                380                 385                 390

tgt ctg gtc aaa gac ttc ttc cca cct gag att gat gtg gag tgg cag     1252
Cys Leu Val Lys Asp Phe Phe Pro Pro Glu Ile Asp Val Glu Trp Gln
            395                 400                 405

agc aat gga cag cag gag cct gag agc aag tac cgc atg acc ccg ccc     1300
Ser Asn Gly Gln Gln Glu Pro Glu Ser Lys Tyr Arg Met Thr Pro Pro
            410                 415                 420

cag ctg gat gaa gat ggg tcc tac ttc cta tac agc aag ctc tcc gtg     1348
Gln Leu Asp Glu Asp Gly Ser Tyr Phe Leu Tyr Ser Lys Leu Ser Val
        425                 430                 435

gac aag agc cgc tgg cag cgg gga gac acc ttc ata tgt gcg gtg atg     1396
Asp Lys Ser Arg Trp Gln Arg Gly Asp Thr Phe Ile Cys Ala Val Met
440                 445                 450                 455
```

17

```
cat gaa gct cta cac aac cac tac aca cag ata tcc ctc tcc cat tct    1444
His Glu Ala Leu His Asn His Tyr Thr Gln Ile Ser Leu Ser His Ser
                460                 465                 470

ccg ggt aaa tga                                                    1456
Pro Gly Lys
```

<210> 17
<211> 474
<212> PRT
<213> Canis familiaris
<223> At location 27, n = unknown

<400> 17

```
Met Glu Ser Val Leu Tyr Trp Val Phe Leu Val Ala Ile Leu Lys Gly
 1               5                  10                  15

Val Gln Gly Asp Val Gln Leu Val Glu Ser Gly Gly Asp Leu Val Lys
            20                  25                  30

Pro Gly Gly Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Phe
            35                  40                  45

Ser Ser Cys Ala Met Ser Trp Val Arg Gln Ser Pro Gly Lys Gly Pro
        50                  55                  60

Gln Trp Val Ala Thr Ile Arg Tyr Asp Gly Ser Asp Ile Tyr Tyr Ala
 65                  70                  75                  80

Asp Ala Val Lys Gly Arg Phe Ser Ile Ser Arg Asp Asn Ala Lys Asn
                85                  90                  95

Thr Val Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
            100                 105                 110

Tyr Tyr Cys Ala Lys Ala Pro Pro Tyr Asp Ser Tyr His Tyr Gly Met
            115                 120                 125

Asp Tyr Trp Gly Pro Gly Thr Ser Leu Phe Val Ser Ser Ala Ser Thr
    130                 135                 140

Thr Ala Pro Ser Val Phe Pro Leu Ala Pro Ser Cys Gly Ser Gln Ser
145                 150                 155                 160

Gly Ser Thr Val Ala Leu Ala Cys Leu Val Ser Gly Tyr Ile Pro Glu
                165                 170                 175
```

18

Pro Val Thr Val Ser Trp Asn Ser Val Ser Leu Thr Ser Gly Val His
          180   185   190

Thr Phe Pro Ser Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser
          195   200   205

Met Val Thr Val Pro Ser Ser Arg Trp Pro Ser Glu Thr Phe Thr Cys
     210   215   220

Asn Val Ala His Pro Ala Thr Asn Thr Lys Val Asp Lys Pro Val Ala
225   230   235   240

Lys Glu Cys Glu Cys Lys Cys Asn Cys Asn Asn Cys Pro Cys Pro Gly
          245   250   255

Cys Gly Leu Leu Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Pro
          260   265   270

Lys Asp Ile Leu Val Thr Ala Arg Thr Pro Thr Val Thr Cys Val Val
          275   280   285

Val Asp Leu Asp Pro Glu Asn Pro Glu Val Gln Ile Ser Trp Phe Val
     290   295   300

Asp Ser Lys Gln Val Gln Thr Ala Asn Thr Gln Pro Arg Glu Glu Gln
305   310   315   320

Ser Asn Gly Thr Tyr Arg Val Val Ser Val Leu Pro Ile Gly His Gln
                    325   330   335

Asp Trp Leu Ser Gly Lys Gln Phe Lys Cys Lys Val Asn Asn Lys Ala
          340   345   350

Leu Pro Ser Pro Ile Glu Glu Ile Ile Ser Lys Thr Pro Gly Gln Ala
          355   360   365

His Gln Pro Asn Val Tyr Val Leu Pro Pro Ser Arg Asp Glu Met Ser
     370   375   380

Lys Asn Thr Val Thr Leu Thr Cys Leu Val Lys Asp Phe Phe Pro Pro
385   390   395   400

Glu Ile Asp Val Glu Trp Gln Ser Asn Gly Gln Gln Glu Pro Glu Ser
               405   410   415

Lys Tyr Arg Met Thr Pro Pro Gln Leu Asp Glu Asp Gly Ser Tyr Phe
          420   425   430

Leu Tyr Ser Lys Leu Ser Val Asp Lys Ser Arg Trp Gln Arg Gly Asp
        435   440   445

Thr Phe Ile Cys Ala Val Met His Glu Ala Leu His Asn His Tyr Thr
        450   455   460

Gln Ile Ser Leu Ser His Ser Pro Gly Lys
465   470

<210> 18
<211> 1456
<212> DNA
<213> Canis familiaris

<220>
<223> At location 1430, n = unknown

<400> 18
tcatttaccc ggagaatggg agagggatat ctgtgtgtag tggttgtgta gagcttcatg 60
catcaccgca catatgaagg tgtctccccg ctgccagcgg ctcttgtcca cggagagctt 120
gctgtatagg aagtaggacc catcttcatc cagctggggc ggggtcatgc ggtacttgct 180
ctcaggctcc tgctgtccat tgctctgcca ctccacatca atctcaggtg ggaagaagtc 240
tttgaccaga caggtcaggg tgaccgtatt cttgctcatc tcatcccgcg atggcggcag 300
gacatacaca ttaggctgat gggcctgccc tggggtcttg agatgatct cctcaatggg 360
ggatgggagg gctttgttgt tgactttgca cttgaactgc ttccctgaaa gccagtcctg 420
gtgcccaatg gggaggacac tgaccacacg gtaggtgcca ttggactgct cctcacgagg 480
ctgcgtgttg gctgtttgca cctgcttact atccacgaac cagctgatct gcacctcagg 540
gttttctggg tccagatcca ccaccacaca agtgactgtg ggtgtccggg cagtcacgag 600
gatgtccttg ggttttgggg gaaagatgaa gaccgaaggc cctcccagca ggccacaacc 660
tgggcatggg cagttgttac agttacactt gcactcgcat tctttggcca ctggcttgtc 720
tactttagtg ttggtggccg ggtgggccac attgcaggtg aaggtctcgc tgggccacct 780
gctggagggc actgtcacca tgctgctgag ggagtagagc cctgaggact gcaggacgga 840
cgggaaggtg tgcacaccgc tggtcaagga gacggaattc caggacacag ttacaggctc 900
ggggatgtag cctgacacca ggcaggccag ggccaccgtg gagccggatt gggacccaca 960
gctggggggcc agtgggaaaa ccgagggggc cgtggtggag gctgacgaca cgaagaggga 1020
agtgccagga ccccaatagt ccataccata gtggtaacta tcgtagggggg gggccttcgc 1080
acaataatac acggccgtgt cctcggctct caggctgttc atctgcagat acaccgtgtt 1140
cttggcgttg tctctggaga tgctgaatcg gcccttcaca gcgtctgcgt agtatatatc 1200
acttccatca taccgaatag ttgcgaccca ctgaggcccc ttccctggag actgacggac 1260
ccagctcatg gcacagctac taaaggtgaa tccagaggcc acacaggaca gtctcaagga 1320
cccccccaggc ttcaccaggt ctcccccaga ctccaccagc tgcacgtcac cctggacacc 1380
ctttaaaata gcgacaagga aaacccagta gagcacagac tccatggtgn tttgtctgtg 1440
ttgtgcctga gcactt   1456

<210> 19

<211> 1453
<212> DNA
<213> Canis familiaris

<220>
<221> CDS
<222> (32)..(1450)

<400> 19
agtgctcagg acaccacaca gacaaatcac c atg gag tct gtg ctc ttc tgg   52
               Met Glu Ser Val Leu Phe Trp
               1   5

gtt ttc ctt gtc act att tta aaa ggt gtc cag ggt gag gta cgt ttg   100
Val Phe Leu Val Thr Ile Leu Lys Gly Val Gln Gly Glu Val Arg Leu
   10   15   20

gtg gag tct gga gga acc ctg gtg aag cct ggg ggg tcc ctg aaa ctc   148
Val Glu Ser Gly Gly Thr Leu Val Lys Pro Gly Gly Ser Leu Lys Leu
  25   30   35

tct tgt gtg gcc tct gga ttc acc ttc aga aga tac tcc atg gac tgg   196
Ser Cys Val Ala Ser Gly Phe Thr Phe Arg Arg Tyr Ser Met Asp Trp
 40   45   50   55

gtc cgc cag gct cca ggc aag agc ctg cag tgg gtc gcc ggg att aac   244
Val Arg Gln Ala Pro Gly Lys Ser Leu Gln Trp Val Ala Gly Ile Asn
       60   65   70

ggt gat ggc aca gga aca tcc tat tca cag act gtg aag ggc cga ttc   292
Gly Asp Gly Thr Gly Thr Ser Tyr Ser Gln Thr Val Lys Gly Arg Phe
      75   80   85

acc atc tcc aga gac aac gcc aag aac acc ctc tat ctg cag ata aac   340
Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr Leu Gln Ile Asn
    90   95   100

agc ctg aga gcc gaa gac tct gct gtg tat tat tgt gcc aag agc tgg   388
Ser Leu Arg Ala Glu Asp Ser Ala Val Tyr Tyr Cys Ala Lys Ser Trp
 105   110   115

tct cgt aat ggg gat ctt gac tac tgg ggc cag gga acc ctg gtc acc   436
Ser Arg Asn Gly Asp Leu Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr
120   125   130   135

gtc tcc tca gcc tcc acc acg gcc ccc tcg gtt ttc cca ctg gcc ccc   484
Val Ser Ser Ala Ser Thr Thr Ala Pro Ser Val Phe Pro Leu Ala Pro
      140   145   150

21

```
agc tgc ggg tcc act tcc ggc tcc acg gtg gcc ctg gcc tgc ctg gtg    532
Ser Cys Gly Ser Thr Ser Gly Ser Thr Val Ala Leu Ala Cys Leu Val
            155               160               165

tca ggc tac ttc ccc gag cct gta act gtg tcc tgg aat tcc ggc tcc    580
Ser Gly Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ser
            170               175               180

ttg acc agc ggt gtg cac acc ttc ccg tcc gtc ctg cag tcc tca ggg    628
Leu Thr Ser Gly Val His Thr Phe Pro Ser Val Leu Gln Ser Ser Gly
        185               190               195

ctc tac tcc ctc agc agc atg gtg aca gtg ccc tcc agc agg tgg ccc    676
Leu Tyr Ser Leu Ser Ser Met Val Thr Val Pro Ser Ser Arg Trp Pro
200               205               210               215

agc gag acc ttc acc tgc aac gtg gcc cac ccg gcc agc aaa act aaa    724
Ser Glu Thr Phe Thr Cys Asn Val Ala His Pro Ala Ser Lys Thr Lys
                220               225               230

gta gac aag cca gtg ccc aaa aga gaa aat gga aga gtt cct cgc cca    772
Val Asp Lys Pro Val Pro Lys Arg Glu Asn Gly Arg Val Pro Arg Pro
            235               240               245

cct gat tgt ccc aaa tgc cca gcc cct gaa atg ctg gga ggg cct tcg    820
Pro Asp Cys Pro Lys Cys Pro Ala Pro Glu Met Leu Gly Gly Pro Ser
            250               255               260

gtc ttc atc ttt ccc ccg aaa ccc aag gac acc ctc ttg att gcc cga    868
Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Thr Leu Leu Ile Ala Arg
        265               270               275

aca cct gag gtc aca tgt gtg gtg gtg gat ctg gac cca gaa gac cct    916
Thr Pro Glu Val Thr Cys Val Val Val Asp Leu Asp Pro Glu Asp Pro
280               285               290               295

gag gtg cag atc agc tgg ttc gtg gac ggt aag cag atg caa aca gcc    964
Glu Val Gln Ile Ser Trp Phe Val Asp Gly Lys Gln Met Gln Thr Ala
                300               305               310

aag act cag cct cgt gag gag cag ttc aat ggc acc tac cgt gtg gtc   1012
Lys Thr Gln Pro Arg Glu Glu Gln Phe Asn Gly Thr Tyr Arg Val Val
            315               320               325

agt gtc ctc ccc att ggg cac cag gac tgg ctc aag ggg aag cag ttc   1060
Ser Val Leu Pro Ile Gly His Gln Asp Trp Leu Lys Gly Lys Gln Phe
            330               335               340
```

22

```
acg tgc aaa gtc aac aac aaa gcc ctc cca tcc ccg atc gag agg acc    1108
Thr Cys Lys Val Asn Asn Lys Ala Leu Pro Ser Pro Ile Glu Arg Thr
    345                 350                 355

atc tcc aag gcc aga ggg caa gcc cat cag ccc agt gtg tat gtc ctg    1156
Ile Ser Lys Ala Arg Gly Gln Ala His Gln Pro Ser Val Tyr Val Leu
360                 365                 370                 375

ccg cca tcc cgg gag gag ttg agc aag aac aca gtc agc ttg aca tgc    1204
Pro Pro Ser Arg Glu Glu Leu Ser Lys Asn Thr Val Ser Leu Thr Cys
                380                 385                 390

ctg atc aaa gac ttc ttc cca cct gac att gat gtg gag tgg cag agc    1252
Leu Ile Lys Asp Phe Phe Pro Pro Asp Ile Asp Val Glu Trp Gln Ser
                395                 400                 405

aat gga cag cag gag cct gag agc aag tac cgc acg acc ccg ccc cag    1300
Asn Gly Gln Gln Glu Pro Glu Ser Lys Tyr Arg Thr Thr Pro Pro Gln
                410                 415                 420

ctg gac gag gac ggg tcc tac ttc ctg tac agc aag ctc tct gtg gac    1348
Leu Asp Glu Asp Gly Ser Tyr Phe Leu Tyr Ser Lys Leu Ser Val Asp
        425                 430                 435

aag agc cgc tgg cag cgg gga gac acc ttc ata tgt gcg gtg atg cat    1396
Lys Ser Arg Trp Gln Arg Gly Asp Thr Phe Ile Cys Ala Val Met His
440                 445                 450                 455

gaa gct cta cac aac cac tac aca cag gaa tcc ctc tcc cat tct ccg    1444
Glu Ala Leu His Asn His Tyr Thr Gln Glu Ser Leu Ser His Ser Pro
                460                 465                 470

ggt aaa tga                                                        1453
Gly Lys


<210> 20
<211> 473
<212> PRT
<213> Canis familiaris

<400> 20
Met Glu Ser Val Leu Phe Trp Val Phe Leu Val Thr Ile Leu Lys Gly
  1               5                  10                  15

Val Gln Gly Glu Val Arg Leu Val Glu Ser Gly Gly Thr Leu Val Lys
            20                  25                  30
```

23

Pro Gly Gly Ser Leu Lys Leu Ser Cys Val Ala Ser Gly Phe Thr Phe
        35   40   45

Arg Arg Tyr Ser Met Asp Trp Val Arg Gln Ala Pro Gly Lys Ser Leu
    50   55   60

Gln Trp Val Ala Gly Ile Asn Gly Asp Gly Thr Gly Thr Ser Tyr Ser
65   70   75   80

Gln Thr Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn
                85   90   95

Thr Leu Tyr Leu Gln Ile Asn Ser Leu Arg Ala Glu Asp Ser Ala Val
        100   105   110

Tyr Tyr Cys Ala Lys Ser Trp Ser Arg Asn Gly Asp Leu Asp Tyr Trp
        115   120   125

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Thr Ala Pro
    130   135   140

Ser Val Phe Pro Leu Ala Pro Ser Cys Gly Ser Thr Ser Gly Ser Thr
145   150   155   160

Val Ala Leu Ala Cys Leu Val Ser Gly Tyr Phe Pro Glu Pro Val Thr
                165   170   175

Val Ser Trp Asn Ser Gly Ser Leu Thr Ser Gly Val His Thr Phe Pro
                180   185   190

Ser Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Met Val Thr
        195   200   205

Val Pro Ser Ser Arg Trp Pro Ser Glu Thr Phe Thr Cys Asn Val Ala
    210   215   220

His Pro Ala Ser Lys Thr Lys Val Asp Lys Pro Val Pro Lys Arg Glu
225   230   235   240

Asn Gly Arg Val Pro Arg Pro Pro Asp Cys Pro Lys Cys Pro Ala Pro
                245   250   255

Glu Met Leu Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Pro Lys
        260   265   270

Asp Thr Leu Leu Ile Ala Arg Thr Pro Glu Val Thr Cys Val Val Val
        275   280   285

24

Asp Leu Asp Pro Glu Asp Pro Glu Val Gln Ile Ser Trp Phe Val Asp
    290   295   300

Gly Lys Gln Met Gln Thr Ala Lys Thr Gln Pro Arg Glu Glu Gln Phe
305   310   315   320

Asn Gly Thr Tyr Arg Val Val Ser Val Leu Pro Ile Gly His Gln Asp
                325   330   335

Trp Leu Lys Gly Lys Gln Phe Thr Cys Lys Val Asn Asn Lys Ala Leu
            340   345   350

Pro Ser Pro Ile Glu Arg Thr Ile Ser Lys Ala Arg Gly Gln Ala His
            355   360   365

Gln Pro Ser Val Tyr Val Leu Pro Pro Ser Arg Glu Glu Leu Ser Lys
    370   375   380

Asn Thr Val Ser Leu Thr Cys Leu Ile Lys Asp Phe Phe Pro Pro Asp
385   390   395   400

Ile Asp Val Glu Trp Gln Ser Asn Gly Gln Gln Glu Pro Glu Ser Lys
                405   410   415

Tyr Arg Thr Thr Pro Pro Gln Leu Asp Glu Asp Gly Ser Tyr Phe Leu
            420   425   430

Tyr Ser Lys Leu Ser Val Asp Lys Ser Arg Trp Gln Arg Gly Asp Thr
            435   440   445

Phe Ile Cys Ala Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
    450   455   460

Glu Ser Leu Ser His Ser Pro Gly Lys
465   470

<210> 21
<211> 1453
<212> DNA
<213> Canis familiaris

<400> 21
tcatttaccc ggagaatggg agagggattc ctgtgtgtag tggttgtgta gagcttcatg 60
catcaccgca catatgaagg tgtctccccg ctgccagcgg ctcttgtcca cagagagctt 120
gctgtacagg aagtaggacc cgtcctcgtc cagctggggc ggggtcgtgc ggtacttgct 180

25

```
ctcaggctcc tgctgtccat tgctctgcca ctccacatca atgtcaggtg ggaagaagtc 240
tttgatcagg catgtcaagc tgactgtgtt cttgctcaac tcctcccggg atggcggcag 300
gacatacaca ctgggctgat gggcttgccc tctggccttg agatggtcc tctcgatcgg 360
ggatgggagg gctttgttgt tgactttgca cgtgaactgc ttcccctttga gccagtcctg 420
gtgcccaatg gggaggacac tgaccacacg gtaggtgcca ttgaactgct cctcacgagg 480
ctgagtcttg gctgtttgca tctgcttacc gtccacgaac cagctgatct gcacctcagg 540
gtcttctggg tccagatcca ccaccacaca tgtgacctca ggtgttcggg caatcaagag 600
ggtgtccttg ggtttcgggg gaaagatgaa gaccgaaggc cctcccagca tttcagggggc 660
tgggcatttg ggacaatcag gtgggcgagg aactcttcca ttttctcttt tgggcactgg 720
cttgtctact ttagttttgc tggccgggtg ggccacgttg caggtgaagg tctcgctggg 780
ccacctgctg gagggcactg tcaccatgct gctgagggag tagagccctg aggactgcag 840
gacggacggg aaggtgtgca caccgctggt caaggagccg gaattccagg acacagttac 900
aggctcgggg aagtagcctg acaccaggca ggccagggcc accgtggagc cggaagtgga 960
cccgcagctg ggggccagtg ggaaaaccga gggggccgtg gtggaggctg aggagacggt 1020
gaccagggtt ccctggcccc agtagtcaag atccccatta cgagaccagc tcttggcaca 1080
ataatacaca gcagagtctt cggctctcag gctgtttatc tgcagataga gggtgttctt 1140
ggcgttgtct ctggagatgg tgaatcggcc cttcacagtc tgtgaatagg atgttcctgt 1200
gccatcaccg ttaatcccgg cgacccactg caggctcttg cctggagcct ggcggaccca 1260
gtccatggag tatcttctga aggtgaatcc agaggccaca caagagagtt tcagggaccc 1320
cccaggcttc accagggttc ctccagactc caccaaacgt acctcaccct ggacaccttt 1380
taaaatagtg acaaggaaaa cccagaagag cacagactcc atggtgattt gtctgtgtgg 1440
tgtcctgagc act                                                   1453


<210> 22
<211> 66
<212> DNA
<213> Canis familiaris

<220>
<221> CDS
<222> (1)..(66)

<400> 22
ccc aaa aga gaa aat gga aga gtt cct cgc cca cct gat tgt ccc aaa    48
Pro Lys Arg Glu Asn Gly Arg Val Pro Arg Pro Pro Asp Cys Pro Lys
  1               5                  10                  15

tgc cca gcc cct gaa atg                                           66
Cys Pro Ala Pro Glu Met
            20


<210> 23
<211> 22
<212> PRT
<213> Canis familiaris
```

26

<400> 23

Pro Lys Arg Glu Asn Gly Arg Val Pro Arg Pro Pro Asp Cys Pro Lys
1   5   10   15

Cys Pro Ala Pro Glu Met
            20

<210> 24
<211> 66
<212> DNA
<213> Canis familiaris

<400> 24
catttcaggg gctgggcatt tgggacaatc aggtgggcga ggaactcttc cattttctct 60
tttggg   66

<210> 25
<211> 938
<212> DNA
<213> Canis familiaris

<220>
<221> CDS
<222> (37)..(753)

<220>
<223> At location 475, n = unknown

<400> 25
ggcacgaggg tccccagaag gcaggatcaa tcagtg atg tcc tcc gac atg gcc   54
                                       Met Ser Ser Asp Met Ala
                                       1   5

tgg tcc cct ctc ctc ctc aca ctc ctc gct cac tgc aca ggg tcc tgg   102
Trp Ser Pro Leu Leu Leu Thr Leu Leu Ala His Cys Thr Gly Ser Trp
            10   15   20

gcc cag gct gtg ttg aat cag ccg gcc tca gta tct ggg gcc ctg ggc   150
Ala Gln Ala Val Leu Asn Gln Pro Ala Ser Val Ser Gly Ala Leu Gly
            25   30   35

cag aag gtc acc atc tcc tgc tct gga gac acg aat gac att gat ata   198
Gln Lys Val Thr Ile Ser Cys Ser Gly Asp Thr Asn Asp Ile Asp Ile
        40   45   50

27

```
ttc ggt gtg aac tgg tac caa caa ctc cca gga aag gcc cct aca gtc     246
Phe Gly Val Asn Trp Tyr Gln Gln Leu Pro Gly Lys Ala Pro Thr Val
 55                  60                  65                  70


ctc gtg gac agt gat ggg gat cga ccc tca ggg gtc cct gac aga ttt     294
Leu Val Asp Ser Asp Gly Asp Arg Pro Ser Gly Val Pro Asp Arg Phe
                 75                  80                  85


tct ggc tcc agt tct ggc aac tca ggc acc ctg acc atc act ggg ctc     342
Ser Gly Ser Ser Ser Gly Asn Ser Gly Thr Leu Thr Ile Thr Gly Leu
                 90                  95                  100


cag gct gag gac gag gct gat tat tac tgt cag tct gtt gat tcc acg     390
Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Val Asp Ser Thr
             105                 110                 115


ctt ggt gtt tac gtg ttc ggc tca gga acc caa ctg act gtc ctt ggt     438
Leu Gly Val Tyr Val Phe Gly Ser Gly Thr Gln Leu Thr Val Leu Gly
             120                 125                 130


cag ccc aag gcc tcc ccc tcg gtc aca ctc ttc ccg ncc tyc tyt gag     486
Gln Pro Lys Ala Ser Pro Ser Val Thr Leu Phe Pro Xaa Xaa Xaa Glu
135                 140                 145                 150


gag ctc ggc gcc aac aag gcc acc ctg gtg tgc ctc atc agc gac ttc     534
Glu Leu Gly Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe
                 155                 160                 165


tac ccc arc ggc gtg acg gtg gcc tgg aag gca gac ggc agc ccc gtc     582
Tyr Pro Xaa Gly Val Thr Val Ala Trp Lys Ala Asp Gly Ser Pro Val
                 170                 175                 180


acc cag ggc gtg gag acc acc aag ccc tcc aag cag agc aac aac aag     630
Thr Gln Gly Val Glu Thr Thr Lys Pro Ser Lys Gln Ser Asn Asn Lys
             185                 190                 195


tac gcg gcc agc agc tac ctg agc ctg acg cct gac aag tgg aaa tct     678
Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Asp Lys Trp Lys Ser
         200                 205                 210


cac agc agc ttc agc tgc ctg gtc acg cat gag ggg agc ccc gtg gaa     726
His Ser Ser Phe Ser Cys Leu Val Thr His Glu Gly Ser Pro Val Glu
215                 220                 225                 230


aaa aag gtg gcc ccc gca aag tgc tct taggttcccg atgccccccg           773
Lys Lys Val Ala Pro Ala Lys Cys Ser
                 235
```

28

cccaccaaag ggggctcaaa gcctcaggac ctccaggagg atcttgcctc ccatctgggt 833

catcccagcc attcccctta aacccaggca acattcaata aagtgttctt tcttcaatca 893

gaaaaaaaaa aaaaaaaaa aaaaaaaaa aaaaaaaaa aaaaa   938

<210> 26
<211> 239
<212> PRT
<213> Canis familiaris
<223> At location 475, n = unknown

<400> 26
Met Ser Ser Asp Met Ala Trp Ser Pro Leu Leu Leu Thr Leu Leu Ala
 1   5   10   15

His Cys Thr Gly Ser Trp Ala Gln Ala Val Leu Asn Gln Pro Ala Ser
                20   25   30

Val Ser Gly Ala Leu Gly Gln Lys Val Thr Ile Ser Cys Ser Gly Asp
        35   40   45

Thr Asn Asp Ile Asp Ile Phe Gly Val Asn Trp Tyr Gln Gln Leu Pro
        50   55   60

Gly Lys Ala Pro Thr Val Leu Val Asp Ser Asp Gly Asp Arg Pro Ser
65   70   75   80

Gly Val Pro Asp Arg Phe Ser Gly Ser Ser Ser Gly Asn Ser Gly Thr
                85   90   95

Leu Thr Ile Thr Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys
            100   105   110

Gln Ser Val Asp Ser Thr Leu Gly Val Tyr Val Phe Gly Ser Gly Thr
            115   120   125

Gln Leu Thr Val Leu Gly Gln Pro Lys Ala Ser Pro Ser Val Thr Leu
        130   135   140

Phe Pro Xaa Xaa Xaa Glu Glu Leu Gly Ala Asn Lys Ala Thr Leu Val
145   150   155   160

Cys Leu Ile Ser Asp Phe Tyr Pro Xaa Gly Val Thr Val Ala Trp Lys
                165   170   175

Ala Asp Gly Ser Pro Val Thr Gln Gly Val Glu Thr Thr Lys Pro Ser

29

```
                180                    185                        190

     Lys Gln Ser Asn Asn Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr
             195                 200                 205


     Pro Asp Lys Trp Lys Ser His Ser Ser Phe Ser Cys Leu Val Thr His
          210                 215                 220


     Glu Gly Ser Pro Val Glu Lys Lys Val Ala Pro Ala Lys Cys Ser
     225                 230                 235
```

<210> 27
<211> 938
<212> DNA
<213> Canis familiaris

<220>
<223> At location 464, n = unknown

<400> 27
```
tttttttttt tttttttttt tttttttttt tttttttttt ttttctgatt gaagaaagaa 60
cactttattg aatgttgcct gggtttaagg ggaatggctg ggatgaccca gatgggaggc 120
aagatcctcc tggaggtcct gaggctttga gcccccttttg gtgggcgggg ggcatcggga 180
acctaagagc actttgcggg ggccaccttt ttttccacgg ggctcccctc atgcgtgacc 240
aggcagctga agctgctgtg agatttccac ttgtcaggcg tcaggctcag gtagctgctg 300
gccgcgtact tgttgttgct ctgcttggag ggcttggtgg tctccacgcc ctgggtgacg 360
gggctgccgt ctgccttcca ggccaccgtc acgccgytgg ggtagaagtc gctgatgagg 420
cacaccaggg tggccttgtt ggcgccgagc tcctcaragr aggncgggaa gagtgtgacc 480
gagggggagg ccttgggctg accaaggaca gtcagttggg ttcctgagcc gaacacgtaa 540
acaccaagcg tggaatcaac agactgacag taataatcag cctcgtcctc agcctggagc 600
ccagtgatgg tcagggtgcc tgagttgcca gaactggagc cagaaaatct gtcagggacc 660
cctgagggtc gatccccatc actgtccacg aggactgtag gggcctttcc tgggagttgt 720
tggtaccagt tcacaccgaa tatatcaatg tcattcgtgt ctccagagca ggagatggtg 780
accttctggc ccagggcccc agatactgag gccggctgat tcaacacagc ctgggcccag 840
gaccctgtgc agtgagcgag gagtgtgagg aggagagggg accaggccat gtcggaggac 900
atcactgatt gatcctgcct tctggggacc ctcgtgcc                        938
```

<210> 28
<211> 578
<212> DNA
<213> Canis familiaris

<220>
<221> CDS
<222> (1)..(423)

<220>
<223> At locations 471, 481, 522 and 549, n = unknown

<400> 28
```
cat caa gat tgg ttt aat ggt aag gag ttc aaa tgt aga gtc aac cac    48
His Gln Asp Trp Phe Asn Gly Lys Glu Phe Lys Cys Arg Val Asn His
  1               5                  10                  15


ata gac ctc ccg tct ccc atc gag agg acc atc tct aag gcc aga ggg    96
Ile Asp Leu Pro Ser Pro Ile Glu Arg Thr Ile Ser Lys Ala Arg Gly
                 20                  25                  30


agg gcc cat aag ccc agt gtg tat gtc ctg ccg cca tcc cca aag gag   144
Arg Ala His Lys Pro Ser Val Tyr Val Leu Pro Pro Ser Pro Lys Glu
             35                  40                  45


ttg tca tcc agt gac aca gtc agc atc acc tgc ctg ata aaa gac ttc   192
Leu Ser Ser Ser Asp Thr Val Ser Ile Thr Cys Leu Ile Lys Asp Phe
         50                  55                  60


tac cca cct gac att gat gtg gag tgg cag agc aat gga cag cag gag   240
Tyr Pro Pro Asp Ile Asp Val Glu Trp Gln Ser Asn Gly Gln Gln Glu
 65                  70                  75                  80


cct gag agc aag tac cgc acg acc ccg ccc cag ctg gac gag gac ggg   288
Pro Glu Ser Lys Tyr Arg Thr Thr Pro Pro Gln Leu Asp Glu Asp Gly
                 85                  90                  95


tcc tac ttc ctg tac agc aag ctc tct gtg gac aag agc cgc tgg cag   336
Ser Tyr Phe Leu Tyr Ser Lys Leu Ser Val Asp Lys Ser Arg Trp Gln
             100                 105                 110


cgg gga gac acc ttc ata tgt gcg gtg atg cat gaa gct cta cac aac   384
Arg Gly Asp Thr Phe Ile Cys Ala Val Met His Glu Ala Leu His Asn
             115                 120                 125


cac tac aca cag aaa tcc ctc tcc cat tct ccg ggt aaa tgagcaacac   433
His Tyr Thr Gln Lys Ser Leu Ser His Ser Pro Gly Lys
             130                 135                 140


gcccggcacc cagcaagccc cccacccttg gctctcanga tccctganga cacctgagcc 493


cctgtccctg tgtacataac cctgggtang cacccatcat gaaataaagc acccancact 553


gccctgggcc cttgcaaaaa aaaaa                                        578
```

<210> 29
<211> 141
<212> PRT
<213> Canis familiaris
<223> At locations 471, 481, 522 and 549, n = unknown

<400> 29
His Gln Asp Trp Phe Asn Gly Lys Glu Phe Lys Cys Arg Val Asn His
 1   5   10   15

Ile Asp Leu Pro Ser Pro Ile Glu Arg Thr Ile Ser Lys Ala Arg Gly
            20   25   30

Arg Ala His Lys Pro Ser Val Tyr Val Leu Pro Pro Ser Pro Lys Glu
        35   40   45

Leu Ser Ser Ser Asp Thr Val Ser Ile Thr Cys Leu Ile Lys Asp Phe
    50   55   60

Tyr Pro Pro Asp Ile Asp Val Glu Trp Gln Ser Asn Gly Gln Gln Glu
65   70   75   80

Pro Glu Ser Lys Tyr Arg Thr Thr Pro Pro Gln Leu Asp Glu Asp Gly
                85   90   95

Ser Tyr Phe Leu Tyr Ser Lys Leu Ser Val Asp Lys Ser Arg Trp Gln
            100   105   110

Arg Gly Asp Thr Phe Ile Cys Ala Val Met His Glu Ala Leu His Asn
            115   120   125

His Tyr Thr Gln Lys Ser Leu Ser His Ser Pro Gly Lys
    130   135   140

<210> 30
<211> 578
<212> DNA
<213> Canis familiaris

<220>
<223> At locations 30, 57, 98 and 108, n = unknown

<400> 30
tttttttttt gcaagggccc agggcagtgn tgggtgcttt atttcatgat gggtgcntac 60
ccagggttat gtacacaggg acaggggctc aggtgtcntc agggatcntg agagccaagg 120
gtggggggct tgctgggtgc cgggcgtgtt gctcatttac ccggagaatg ggagagggat 180

```
ttctgtgtgt agtggttgtg tagagcttca tgcatcaccg cacatatgaa ggtgtctccc 240
cgctgccagc ggctcttgtc cacagagagc ttgctgtaca ggaagtagga cccgtcctcg 300
tccagctggg gcggggtcgt gcggtacttg ctctcaggct cctgctgtcc attgctctgc 360
cactccacat caatgtcagg tgggtagaag tcttttatca ggcaggtgat gctgactgtg 420
tcactggatg acaactcctt tggggatggc ggcaggacat acacactggg cttatgggcc 480
ctccctctgg ccttagagat ggtcctctcg atgggagacg ggaggtctat gtggttgact 540
ctacatttga actccttacc attaaaccaa tcttgatg                          578
```

<210> 31
<211> 1364
<212> DNA
<213> Canis familiaris

<220>
<221> CDS
<222> (59)..(1183)

<400> 31

```
ggcacgaggc cgattcacca tttccagaga caatgtcgag aacacgctgt atctgcag      58

atg aac agc ctg aga gct gag gat acg gcc ctg tat tac tgt aca agt      106
Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys Thr Ser
  1               5                  10                  15

ggg tta tgg atc aac tgg tac ggt ccg aat ttt gac tcc tgg ggc cag      154
Gly Leu Trp Ile Asn Trp Tyr Gly Pro Asn Phe Asp Ser Trp Gly Gln
                 20                  25                  30

gga acc ctg gtc acc gtc tcc tca gcc tcc acc acg gcc ccc tcg gtt      202
Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Thr Ala Pro Ser Val
             35                  40                  45

ttc cca ctg gcc ccc agc tgc ggg tcc act tcc ggc tcc acg gtg gcc      250
Phe Pro Leu Ala Pro Ser Cys Gly Ser Thr Ser Gly Ser Thr Val Ala
         50                  55                  60

ctg gcc tgc ctg gtg tca ggc tac ttc ccc gag cct gta act gtg tcc      298
Leu Ala Cys Leu Val Ser Gly Tyr Phe Pro Glu Pro Val Thr Val Ser
 65                  70                  75                  80

tgg aat tcc ggc tcc ttg acc agc ggt gtg cac acc ttc ccg tcc gtc      346
Trp Asn Ser Gly Ser Leu Thr Ser Gly Val His Thr Phe Pro Ser Val
                 85                  90                  95

ctg cag tcc tca ggg ctc tac tcc ctc agc agc atg gtg aca gtg ccc      394
Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Met Val Thr Val Pro
                100                 105                 110
```

```
tcc agc agg tgg ccc agc gag acc ttc acc tgc aac gtg gcc cac ccg      442
Ser Ser Arg Trp Pro Ser Glu Thr Phe Thr Cys Asn Val Ala His Pro
        115                 120                 125

gcc agc aaa act aaa gta gac aag cca gtg ccc aaa aga gaa aat gga      490
Ala Ser Lys Thr Lys Val Asp Lys Pro Val Pro Lys Arg Glu Asn Gly
        130                 135                 140

aga gtt cct cgc cca cct gat tgt ccc aaa tgc cca acc cct gaa atg      538
Arg Val Pro Arg Pro Pro Asp Cys Pro Lys Cys Pro Thr Pro Glu Met
145                 150                 155                 160

ctg gga ggg cct tcg gtc ttc atc ttt ccc ccg aaa ccc aag gac acc      586
Leu Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Thr
                165                 170                 175

ctc ttg att gcc cga aca cct gag gtc aca tgt gtg gtg gtg gat ctg      634
Leu Leu Ile Ala Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Leu
                180                 185                 190

gac cca gaa gac cct gag gtg cag atc agc tgg ttc gtg gac ggt aag      682
Asp Pro Glu Asp Pro Glu Val Gln Ile Ser Trp Phe Val Asp Gly Lys
                195                 200                 205

cag atg caa aca gcc aag act cag cct cgt gag gag cag ttc aat ggc      730
Gln Met Gln Thr Ala Lys Thr Gln Pro Arg Glu Glu Gln Phe Asn Gly
        210                 215                 220

acc tac cgt gtg gtc agt gtc ctc ccc att ggg cac cag gac tgg ctc      778
Thr Tyr Arg Val Val Ser Val Leu Pro Ile Gly His Gln Asp Trp Leu
225                 230                 235                 240

aag ggg aag cag ttc acg tgc aaa gtc aac aac aaa gcc ctc cca tcc      826
Lys Gly Lys Gln Phe Thr Cys Lys Val Asn Asn Lys Ala Leu Pro Ser
                245                 250                 255

cca atc gag agg acc atc tcc aag gcc aga ggg cag gcc cat caa ccc      874
Pro Ile Glu Arg Thr Ile Ser Lys Ala Arg Gly Gln Ala His Gln Pro
                260                 265                 270

agt gtg tat gtc ctg ccg cca tcc cgg gag gag ttg agc aag aac aca      922
Ser Val Tyr Val Leu Pro Pro Ser Arg Glu Glu Leu Ser Lys Asn Thr
                275                 280                 285

gtc agc ttg aca tgc ctg atc aaa gac ttc ttc cca cct gac att gat      970
Val Ser Leu Thr Cys Leu Ile Lys Asp Phe Phe Pro Pro Asp Ile Asp
        290                 295                 300
```

34

```
gtg gag tgg cag agc aat gga cag cag gag cct gag agc aag tac cgc    1018
Val Glu Trp Gln Ser Asn Gly Gln Gln Glu Pro Glu Ser Lys Tyr Arg
305                 310             315                 320


acg acc ccg ccc cag ctg gac gag gac ggg tcc tac ttc ctg tac agc    1066
Thr Thr Pro Pro Gln Leu Asp Glu Asp Gly Ser Tyr Phe Leu Tyr Ser
                325             330             335


aag ctc tct gtg gac aag agc cgc tgg cag cgg gga gac acc ttc ata    1114
Lys Leu Ser Val Asp Lys Ser Arg Trp Gln Arg Gly Asp Thr Phe Ile
            340             345             350


tgt gcg gtg atg cat gaa gct tta cac aac cac tac aca cag aaa tcc    1162
Cys Ala Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
            355             360             365


ctc tcc cat tct ccg ggt aaa tgagcaacac gcccggcacc cagcaagccc       1213
Leu Ser His Ser Pro Gly Lys
        370             375


cccacccttg ctttcagga tcccatgagg atgcctgagc ccccatccct gtgtacataa  1273

ccccgggtag gcacctggca tgaaataaag cacccagtac tgccctggaa aaaaaaaaaa  1333

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa a                                 1364



<210> 32
<211> 375
<212> PRT
<213> Canis familiaris

<400> 32
Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys Thr Ser
 1               5               10                  15


Gly Leu Trp Ile Asn Trp Tyr Gly Pro Asn Phe Asp Ser Trp Gly Gln
            20              25              30


Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Thr Ala Pro Ser Val
            35              40              45


Phe Pro Leu Ala Pro Ser Cys Gly Ser Thr Ser Gly Ser Thr Val Ala
    50              55              60


Leu Ala Cys Leu Val Ser Gly Tyr Phe Pro Glu Pro Val Thr Val Ser
 65             70              75              80
```

35

Trp Asn Ser Gly Ser Leu Thr Ser Gly Val His Thr Phe Pro Ser Val
                85   90   95

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Met Val Thr Val Pro
                100   105   110

Ser Ser Arg Trp Pro Ser Glu Thr Phe Thr Cys Asn Val Ala His Pro
                115   120   125

Ala Ser Lys Thr Lys Val Asp Lys Pro Val Pro Lys Arg Glu Asn Gly
        130   135   140

Arg Val Pro Arg Pro Pro Asp Cys Pro Lys Cys Pro Thr Pro Glu Met
145   150   155   160

Leu Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Thr
                165   170   175

Leu Leu Ile Ala Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Leu
                180   185   190

Asp Pro Glu Asp Pro Glu Val Gln Ile Ser Trp Phe Val Asp Gly Lys
                195   200   205

Gln Met Gln Thr Ala Lys Thr Gln Pro Arg Glu Glu Gln Phe Asn Gly
        210   215   220

Thr Tyr Arg Val Val Ser Val Leu Pro Ile Gly His Gln Asp Trp Leu
225   230   235   240

Lys Gly Lys Gln Phe Thr Cys Lys Val Asn Asn Lys Ala Leu Pro Ser
                245   250   255

Pro Ile Glu Arg Thr Ile Ser Lys Ala Arg Gly Gln Ala His Gln Pro
                260   265   270

Ser Val Tyr Val Leu Pro Pro Ser Arg Glu Glu Leu Ser Lys Asn Thr
                275   280   285

Val Ser Leu Thr Cys Leu Ile Lys Asp Phe Phe Pro Pro Asp Ile Asp
        290   295   300

Val Glu Trp Gln Ser Asn Gly Gln Gln Glu Pro Glu Ser Lys Tyr Arg
305   310   315   320

Thr Thr Pro Pro Gln Leu Asp Glu Asp Gly Ser Tyr Phe Leu Tyr Ser
                325   330   335

36

Lys Leu Ser Val Asp Lys Ser Arg Trp Gln Arg Gly Asp Thr Phe Ile
        340   345   350

Cys Ala Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
        355   360   365

Leu Ser His Ser Pro Gly Lys
    370   375

<210> 33
<211> 1364
<212> DNA
<213> Canis familiaris

<400> 33
ttttttttt ttttttttt ttttttttt ttttttttt tttccagggc agtactgggt 60
gctttatttc atgccaggtg cctacccggg gttatgtaca cagggatggg ggctcaggca 120
tcctcatggg atcctgaaag ccaaggtggg ggggcttgct gggtgccggg cgtgttgctc 180
atttacccgg agaatgggag agggatttct gtgtgtagtg gttgtgtaaa gcttcatgca 240
tcaccgcaca tatgaaggtg tctccccgct gccagcggct cttgtccaca gagagcttgc 300
tgtacaggaa gtaggacccg tcctcgtcca gctggggcgg ggtcgtgcgg tacttgctct 360
caggctcctg ctgtccattg ctctgccact ccacatcaat gtcaggtggg aagaagtctt 420
tgatcaggca tgtcaagctg actgtgttct tgctcaactc ctccccgggat ggcggcagga 480
catacacact gggttgatgg gcctgccctc tggccttgga gatggtcctc tcgattgggg 540
atgggagggc tttgttgttg actttgcacg tgaactgctt ccccttgagc cagtcctggt 600
gcccaatggg gaggacactg accacacggt aggtgccatt gaactgctcc tcacgaggct 660
gagtcttggc tgtttgcatc tgcttaccgt ccacgaacca gctgatctgc acctcagggt 720
cttctgggtc cagatccacc accacacatg tgacctcagg tgttcgggca atcaagaggg 780
tgtccttggg tttcggggga aagatgaaga ccgaaggccc tcccagcatt tcaggggttg 840
ggcatttggg acaatcaggt gggcgaggaa ctcttccatt ttctcttttg ggcactggct 900
tgtctacttt agttttgctg gccgggtggg ccacgttgca ggtgaaggtc tcgctgggcc 960
acctgctgga gggcactgtc accatgctgc tgagggagta gagccctgag gactgcagga 1020
cggacgggaa ggtgtgcaca ccgctggtca aggagccgga attccaggac acagttacag 1080
gctcggggaa gtagcctgac accaggcagg ccagggccac cgtggagccg gaagtggacc 1140
cgcagctggg ggccagtggg aaaaccgagg gggccgtggt ggaggctgag gagacggtga 1200
ccagggttcc ctggccccag gagtcaaaat tcggaccgta ccagttgatc cataacccac 1260
ttgtacagta atacagggcc gtatcctcag ctctcaggct gttcatctgc agatacagcg 1320
tgttctcgac attgtctctg gaaatggtga atcggcctcg tgcc 1364

<210> 34
<211> 1168
<212> DNA
<213> Canis familiaris

<220>
<221> CDS
<222> (48)..(1166)

<400> 34
ccaggtgacc ccattcagtg ctcaggacac aacacagaca aaccacc atg gag tct   56
                                                    Met Glu Ser
                                                     1

gtg ctc tgc tgg gtt ttc ctt gtc tct att tta aaa ggt gtc cag ggt   104
Val Leu Cys Trp Val Phe Leu Val Ser Ile Leu Lys Gly Val Gln Gly
          5   10   15

gag gtg caa ctg gtg gag tct ggg gga gac ctg gtg aag cct ggg ggg   152
Glu Val Gln Leu Val Glu Ser Gly Gly Asp Leu Val Lys Pro Gly Gly
 20   25   30   35

tcc ttg aga ctg tcc tgt gtg gcc tct gga ttc acc ttc agt gac tat   200
Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Phe Ser Asp Tyr
                 40   45   50

ggc atg agt tgg gtc cgt cag tct cca ggg aag ggg ctg cag tgg gtc   248
Gly Met Ser Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Gln Trp Val
             55   60   65

gca gct gtt agc aat cgt gga gat act tac tac gca gac gct gtg aag   296
Ala Ala Val Ser Asn Arg Gly Asp Thr Tyr Tyr Ala Asp Ala Val Lys
             70   75   80

ggc cga ttc acc atc tcc aga gac aac gcc aag aac acg ctg tat ctc   344
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr Leu
     85   90   95

cag atg agc agc ctg aaa gcc gag gac acg gca atc tat cac tgt gtg   392
Gln Met Ser Ser Leu Lys Ala Glu Asp Thr Ala Ile Tyr His Cys Val
100   105   110   115

acg gga gta tgg ccg cga cat tat tat ggt atg gac cac tgg ggc aat   440
Thr Gly Val Trp Pro Arg His Tyr Tyr Gly Met Asp His Trp Gly Asn
                120   125   130

ggc acc tca ctc ttc gtg tcc tca gcc tcc acc acg gcc ccc tcg gtt   488
Gly Thr Ser Leu Phe Val Ser Ser Ala Ser Thr Thr Ala Pro Ser Val
                135   140   145

ttc cca ctg gcc ccc agc tgc ggg tcc act tcc ggc tcc acg gtg gcc   536
Phe Pro Leu Ala Pro Ser Cys Gly Ser Thr Ser Gly Ser Thr Val Ala
            150   155   160

38

```
ctg gcc tgc ctg gtg tca ggc tac ttc ccc gag cct gta act gtg tcc    584
Leu Ala Cys Leu Val Ser Gly Tyr Phe Pro Glu Pro Val Thr Val Ser
    165                 170                 175

tgg aat tcc ggc tcc ttg acc agc ggt gtg cac acc ttc ccg tcc gtc    632
Trp Asn Ser Gly Ser Leu Thr Ser Gly Val His Thr Phe Pro Ser Val
180                 185                 190                 195

ctg cag tcc tca ggg ctc tac tcc ctc agc agc acg gtg aca gtg ccc    680
Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Thr Val Thr Val Pro
                200                 205                 210

tcc agc agg tgg ccc agc gag acc ttc acc tgc aac gtg gtc cac ccg    728
Ser Ser Arg Trp Pro Ser Glu Thr Phe Thr Cys Asn Val Val His Pro
            215                 220                 225

gcc agc aac act aaa gta gac aag cca gtg ccc aaa gag tcc acc tgc    776
Ala Ser Asn Thr Lys Val Asp Lys Pro Val Pro Lys Glu Ser Thr Cys
        230                 235                 240

aag tgt ata tcc cca tgc cca gtc cct gaa tca ctg gga ggg cct tcg    824
Lys Cys Ile Ser Pro Cys Pro Val Pro Glu Ser Leu Gly Gly Pro Ser
    245                 250                 255

gtc ttc atc ttt ccc ccg aaa ccc aag gac atc ctc agg att acc cga    872
Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Ile Leu Arg Ile Thr Arg
260                 265                 270                 275

aca ccc gag atc acc tgt gtg gtg tta gat ctg ggc cgt gag gac cct    920
Thr Pro Glu Ile Thr Cys Val Val Leu Asp Leu Gly Arg Glu Asp Pro
                280                 285                 290

gag gtg cag atc agc tgg ttc gtg gat ggt aag gag gtg cac aca gcc    968
Glu Val Gln Ile Ser Trp Phe Val Asp Gly Lys Glu Val His Thr Ala
            295                 300                 305

aag acg cag cct cgt gag cag cag ttc aac agc acc tac cgt gtg gtc    1016
Lys Thr Gln Pro Arg Glu Gln Gln Phe Asn Ser Thr Tyr Arg Val Val
        310                 315                 320

agc gtc ctc ccc att gag cac cag gac tgg ctc acc gga aag gag ttc    1064
Ser Val Leu Pro Ile Glu His Gln Asp Trp Leu Thr Gly Lys Glu Phe
    325                 330                 335

aag tgc aga gtc aac cac ata ggc ccc ccg tcc ccc atc gag agg act    1112
Lys Cys Arg Val Asn His Ile Gly Pro Pro Ser Pro Ile Glu Arg Thr
340                 345                 350                 355
```

39

```
atc tcc aaa gcc aga ggg caa gcc cat cag ccc agt gtg tat gtc ctg      1160
Ile Ser Lys Ala Arg Gly Gln Ala His Gln Pro Ser Val Tyr Val Leu
            360                 365                 370

ccg cca tc                                                            1168
Pro Pro
```

<210> 35
<211> 373
<212> PRT
<213> Canis familiaris

<400> 35

```
Met Glu Ser Val Leu Cys Trp Val Phe Leu Val Ser Ile Leu Lys Gly
 1               5                  10                  15

Val Gln Gly Glu Val Gln Leu Val Glu Ser Gly Gly Asp Leu Val Lys
            20                  25                  30

Pro Gly Gly Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Phe
            35                  40                  45

Ser Asp Tyr Gly Met Ser Trp Val Arg Gln Ser Pro Gly Lys Gly Leu
    50                  55                  60

Gln Trp Val Ala Ala Val Ser Asn Arg Gly Asp Thr Tyr Tyr Ala Asp
65                  70                  75                  80

Ala Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr
                85                  90                  95

Leu Tyr Leu Gln Met Ser Ser Leu Lys Ala Glu Asp Thr Ala Ile Tyr
            100                 105                 110

His Cys Val Thr Gly Val Trp Pro Arg His Tyr Tyr Gly Met Asp His
            115                 120                 125

Trp Gly Asn Gly Thr Ser Leu Phe Val Ser Ser Ala Ser Thr Thr Ala
    130                 135                 140

Pro Ser Val Phe Pro Leu Ala Pro Ser Cys Gly Ser Thr Ser Gly Ser
145                 150                 155                 160

Thr Val Ala Leu Ala Cys Leu Val Ser Gly Tyr Phe Pro Glu Pro Val
                165                 170                 175
```

```
Thr Val Ser Trp Asn Ser Gly Ser Leu Thr Ser Gly Val His Thr Phe
            180                 185                 190

Pro Ser Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Thr Val
            195                 200                 205

Thr Val Pro Ser Ser Arg Trp Pro Ser Glu Thr Phe Thr Cys Asn Val
            210                 215                 220

Val His Pro Ala Ser Asn Thr Lys Val Asp Lys Pro Val Pro Lys Glu
225                     230                 235                 240

Ser Thr Cys Lys Cys Ile Ser Pro Cys Pro Val Pro Glu Ser Leu Gly
                245                 250                 255

Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Ile Leu Arg
            260                 265                 270

Ile Thr Arg Thr Pro Glu Ile Thr Cys Val Val Leu Asp Leu Gly Arg
            275                 280                 285

Glu Asp Pro Glu Val Gln Ile Ser Trp Phe Val Asp Gly Lys Glu Val
            290                 295                 300

His Thr Ala Lys Thr Gln Pro Arg Glu Gln Gln Phe Asn Ser Thr Tyr
305                     310                 315                 320

Arg Val Val Ser Val Leu Pro Ile Glu His Gln Asp Trp Leu Thr Gly
                325                 330                 335

Lys Glu Phe Lys Cys Arg Val Asn His Ile Gly Pro Pro Ser Pro Ile
            340                 345                 350

Glu Arg Thr Ile Ser Lys Ala Arg Gly Gln Ala His Gln Pro Ser Val
            355                 360                 365

Tyr Val Leu Pro Pro
            370
```

41

```
ctctcgatgg gggacggggg gcctatgtgg ttgactctgc acttgaactc ctttccggtg 120
agccagtcct ggtgctcaat ggggaggacg ctgaccacac ggtaggtgct gttgaactgc 180
tgctcacgag gctgcgtctt ggctgtgtgc acctccttac catccacgaa ccagctgatc 240
tgcacctcag ggtcctcacg gcccagatct aacaccacac aggtgatctc gggtgttcgg 300
gtaatcctga ggatgtcctt gggtttcggg ggaaagatga agaccgaagg ccctcccagt 360
gattcaggga ctgggcatgg ggatatacac ttgcaggtgg actctttggg cactggcttg 420
tctactttag tgttgctggc cgggtggacc acgttgcagg tgaaggtctc gctgggccac 480
ctgctggagg gcactgtcac cgtgctgctg agggagtaga gccctgagga ctgcaggacg 540
gacgggaagg tgtgcacacc gctggtcaag gagccggaat tccaggacac agttacaggc 600
tcggggaagt agcctgacac caggcaggcc agggccaccg tggagccgga agtggacccg 660
cagctggggg ccagtgggaa aaccgagggg gccgtggtgg aggctgagga cacgaagagt 720
gaggtgccat tgccccagtg gtccatacca taataatgtc gcggccatac tcccgtcaca 780
cagtgataga ttgccgtgtc ctcggctttc aggctgctca tctggagata cagcgtgttc 840
ttggcgttgt ctctggagat ggtgaatcgg cccttcacag cgtctgcgta gtaagtatct 900
ccacgattgc taacagctgc gacccactgc agccccttcc ctggagactg acggacccaa 960
ctcatgccat agtcactgaa ggtgaatcca gaggccacac aggacagtct caaggacccc 1020
ccaggcttca ccaggtctcc cccagactcc accagttgca cctcaccctg gacacctttt 1080
aaaatagaga caaggaaaac ccagcagagc acagactcca tggtggtttg tctgtgttgt 1140
gtcctgagca ctgaatgggg tcacctgg                                    1168


<210> 37
<211> 1059
<212> DNA
<213> Canis familiaris

<220>
<221> CDS
<222> (1)..(1056)

<400> 37
tgg ccg cga cat tat tat ggt atg gac cac tgg ggc aat ggc acc tca    48
Trp Pro Arg His Tyr Tyr Gly Met Asp His Trp Gly Asn Gly Thr Ser
  1               5                   10                  15


ctc ttc gtg tcc tca gcc tcc acc acg gcc ccc tcg gtt ttc cca ctg    96
Leu Phe Val Ser Ser Ala Ser Thr Thr Ala Pro Ser Val Phe Pro Leu
             20                  25                  30


gcc ccc agc tgc ggg tcc act tcc ggc tcc acg gtg gcc ctg gcc tgc   144
Ala Pro Ser Cys Gly Ser Thr Ser Gly Ser Thr Val Ala Leu Ala Cys
         35                  40                  45


ctg gtg tca ggc tac ttc ccc gag cct gta act gtg tcc tgg aat tcc   192
Leu Val Ser Gly Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
     50                  55                  60


gac tcc ttg acc agc ggt gtg cac acc ttc ccg tcc gtc ctg cag tcc   240
```

42

```
Asp Ser Leu Thr Ser Gly Val His Thr Phe Pro Ser Val Leu Gln Ser
 65                  70                  75                  80


tca ggg ctc tac tcc ctc agc agc acg gtg aca gtg ccc tcc agc agg    288
Ser Gly Leu Tyr Ser Leu Ser Ser Thr Val Thr Val Pro Ser Ser Arg
                 85                  90                  95


tgg ccc agc gag acc ttc acc tgc aac gtg gtc cac ccg gcc agc aac    336
Trp Pro Ser Glu Thr Phe Thr Cys Asn Val Val His Pro Ala Ser Asn
                 100                 105                 110


act aaa gta gac aag cca gtg ccc aaa gag tcc acc tgc aag tgt ata    384
Thr Lys Val Asp Lys Pro Val Pro Lys Glu Ser Thr Cys Lys Cys Ile
                 115                 120                 125


tcc cca tgc cca gtc cct gaa tca ctg gga ggg cct tcg gtc ttc atc    432
Ser Pro Cys Pro Val Pro Glu Ser Leu Gly Gly Pro Ser Val Phe Ile
             130                 135                 140


ttt ccc ccg aaa ccc aag gac atc ctc agg att acc cga aca ccc gag    480
Phe Pro Pro Lys Pro Lys Asp Ile Leu Arg Ile Thr Arg Thr Pro Glu
145                 150                 155                 160


atc acc tgt gtg gtg tta gat ctg ggc cgt gag gac cct gag gtg cag    528
Ile Thr Cys Val Val Leu Asp Leu Gly Arg Glu Asp Pro Glu Val Gln
                 165                 170                 175


atc agc tgg ttc gtg gat ggt aag gag gtg cac aca gcc aag acg cag    576
Ile Ser Trp Phe Val Asp Gly Lys Glu Val His Thr Ala Lys Thr Gln
                 180                 185                 190


cct cgt gag cag cag ttc aac agc acc tac cgt gtg gtc agc gtc ctc    624
Pro Arg Glu Gln Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu
                 195                 200                 205


ccc att gag cac cag gac tgg ctc acc gga aag gag ttc aag tgc aga    672
Pro Ile Glu His Gln Asp Trp Leu Thr Gly Lys Glu Phe Lys Cys Arg
             210                 215                 220


gtc aac cac ata ggc ctc ccg tcc ccc atc gag agg act atc tcc aaa    720
Val Asn His Ile Gly Leu Pro Ser Pro Ile Glu Arg Thr Ile Ser Lys
225                 230                 235                 240


gcc aga ggg caa gcc cat cag ccc agt gtg tat gtc ctg cca cca tcc    768
Ala Arg Gly Gln Ala His Gln Pro Ser Val Tyr Val Leu Pro Pro Ser
                 245                 250                 255


cca aag gag ttg tca tcc agt gac acg gtc acc ctg acc tgc ctg atc    816
```

43

```
Pro Lys Glu Leu Ser Ser Ser Asp Thr Val Thr Leu Thr Cys Leu Ile
        260                 265                 270

aaa gac ttc ttc cca cct gag att gat gtg gag tgg cag agc aat gga    864
Lys Asp Phe Phe Pro Pro Glu Ile Asp Val Glu Trp Gln Ser Asn Gly
        275                 280                 285

cag ccg gag ccc gag agc aag tac cac acg act gcg ccc cag ctg gac    912
Gln Pro Glu Pro Glu Ser Lys Tyr His Thr Thr Ala Pro Gln Leu Asp
        290                 295                 300

gag gac ggg tcc tac ttc ctg tac agc aag ctc tct gtg gac aag agc    960
Glu Asp Gly Ser Tyr Phe Leu Tyr Ser Lys Leu Ser Val Asp Lys Ser
305                 310                 315                 320

cgc tgg cag cag gga gac ccc ttc aca tgt gcg gtg atg cat gaa gct   1008
Arg Trp Gln Gln Gly Asp Pro Phe Thr Cys Ala Val Met His Glu Ala
                325                 330                 335

cta cag aac cac tac aca gat cta tcc ctc tcc cat tct ccg ggt aaa   1056
Leu Gln Asn His Tyr Thr Asp Leu Ser Leu Ser His Ser Pro Gly Lys
                340                 345                 350

tga                                                                1059


<210> 38
<211> 352
<212> PRT
<213> Canis familiaris

<400> 38
Trp Pro Arg His Tyr Tyr Gly Met Asp His Trp Gly Asn Gly Thr Ser
  1               5                  10                  15

Leu Phe Val Ser Ser Ala Ser Thr Thr Ala Pro Ser Val Phe Pro Leu
                20                  25                  30

Ala Pro Ser Cys Gly Ser Thr Ser Gly Ser Thr Val Ala Leu Ala Cys
            35                  40                  45

Leu Val Ser Gly Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
        50                  55                  60

Asp Ser Leu Thr Ser Gly Val His Thr Phe Pro Ser Val Leu Gln Ser
65                  70                  75                  80

Ser Gly Leu Tyr Ser Leu Ser Ser Thr Val Thr Val Pro Ser Ser Arg
```

44

Trp Pro Ser Glu Thr Phe Thr Cys Asn Val Val His Pro Ala Ser Asn
        100   105   110

Thr Lys Val Asp Lys Pro Val Pro Lys Glu Ser Thr Cys Lys Cys Ile
        115   120   125

Ser Pro Cys Pro Val Pro Glu Ser Leu Gly Gly Pro Ser Val Phe Ile
        130   135   140

Phe Pro Pro Lys Pro Lys Asp Ile Leu Arg Ile Thr Arg Thr Pro Glu
145   150   155   160

Ile Thr Cys Val Val Leu Asp Leu Gly Arg Glu Asp Pro Glu Val Gln
                165   170   175

Ile Ser Trp Phe Val Asp Gly Lys Glu Val His Thr Ala Lys Thr Gln
            180   185   190

Pro Arg Glu Gln Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu
        195   200   205

Pro Ile Glu His Gln Asp Trp Leu Thr Gly Lys Glu Phe Lys Cys Arg
        210   215   220

Val Asn His Ile Gly Leu Pro Ser Pro Ile Glu Arg Thr Ile Ser Lys
225   230   235   240

Ala Arg Gly Gln Ala His Gln Pro Ser Val Tyr Val Leu Pro Pro Ser
            245   250   255

Pro Lys Glu Leu Ser Ser Ser Asp Thr Val Thr Leu Thr Cys Leu Ile
        260   265   270

Lys Asp Phe Phe Pro Pro Glu Ile Asp Val Glu Trp Gln Ser Asn Gly
        275   280   285

Gln Pro Glu Pro Glu Ser Lys Tyr His Thr Thr Ala Pro Gln Leu Asp
    290   295   300

Glu Asp Gly Ser Tyr Phe Leu Tyr Ser Lys Leu Ser Val Asp Lys Ser
305   310   315   320

Arg Trp Gln Gln Gly Asp Pro Phe Thr Cys Ala Val Met His Glu Ala
            325   330   335

Leu Gln Asn His Tyr Thr Asp Leu Ser Leu Ser His Ser Pro Gly Lys

<210> 39
<211> 1059
<212> DNA
<213> Canis familiaris

<400> 39
tcatttaccc ggagaatggg agagggatag atctgtgtag tggttctgta gagcttcatg 60
catcaccgca catgtgaagg ggtctccctg ctgccagcgg ctcttgtcca cagagagctt 120
gctgtacagg aagtaggacc cgtcctcgtc cagctggggc gcagtcgtgt ggtacttgct 180
ctcgggctcc ggctgtccat tgctctgcca ctccacatca atctcaggtg ggaagaagtc 240
tttgatcagg caggtcaggg tgaccgtgtc actggatgac aactcctttg gggatggtgg 300
caggacatac acactgggct gatgggcttg ccctctggct ttggagatag tcctctcgat 360
gggggacggg aggcctatgt ggttgactct gcacttgaac tcctttccgg tgagccagtc 420
ctggtgctca atggggagga cgctgaccac acggtaggtg ctgttgaact gctgctcacg 480
aggctgcgtc ttggctgtgt gcacctcctt accatccacg aaccagctga tctgcacctc 540
agggtcctca cggcccagat ctaacaccac acaggtgatc tcgggtgttc gggtaatcct 600
gaggatgtcc ttgggtttcg ggggaaagat gaagaccgaa ggccctccca gtgattcagg 660
gactgggcat ggggatatac acttgcaggt ggactctttg ggcactggct tgtctacttt 720
agtgttgctg gccgggtgga ccacgttgca ggtgaaggtc tcgctgggcc acctgctgga 780
gggcactgtc accgtgctgc tgagggagta gagccctgag gactgcagga cggacgggaa 840
ggtgtgcaca ccgctggtca aggagtcgga attccaggac acagttacag gctcggggaa 900
gtagcctgac accaggcagg ccagggccac cgtggagccg gaagtggacc cgcagctggg 960
ggccagtggg aaaaccgagg gggccgtggt ggaggctgag gacacgaaga gtgaggtgcc 1020
attgccccag tggtccatac cataataatg tcgcggcca   1059

<210> 40
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
     Primer

<220>
<223> At locations 15 and 21, n = unknown

<400> 40
caycargayt ggytnaaygg naargartty aartgy   36

<210> 41
<211> 28

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Primer

<400> 41
gccctccagc aggtggccca gcgagacc   28

<210> 42
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Primer

<400> 42
ggggatggcg gcaggacata cac   23

<210> 43
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Primer

<400> 43
tttacccgga gaatgggaga ggg   23

<210> 44
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Primer

<400> 44
ggtctgcgtg ggccacctgc tggagggc   28

47

<210> 45
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Primer

<400> 45
gggtggggggg cttgctgggt gccgggcg   28

<210> 46
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Primer

<400> 46
ccaggtgacc ccattcagtg ctcaggacac   30

<210> 47
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Primer

<400> 47
ctgtgtgacg ggagtatggc cgcgac   26

<210> 48
<211> 483
<212> DNA
<213> Canis familiaris

<220>
<223> At location 470, n = unknown

48

<400> 48

```
cttatttgga catggaaccc cccagagggc gccagcccga attgcacctt acggtatttt 60
agtcattttg acaacaaaca ggataagaaa attgctcctg aaactcatcg ttcaaaagaa 120
gtacccctga atgagaggat ttgtctgcaa gtggggtccc agtgcagcac caatgaaagt 180
gacaatccta gcattttggt ggaaaagtgc accccaccac ctgaaggtgg tcctgagtcg 240
gctgtgactg agctacaatg tgtttggcac aacctgagct acatgaagtg tacttggctt 300
cctggaagga atacaagccc tgacaccaac tatactctct actattggca cagcagcctg 360
ggaaaaattc ttcaatgcga agacatctat agagaaggtc aacacattgg ttgttccttt 420
gctctgacta atttgaagga ttccagtttt gaacaacaca gtgtccagan gatggtcaag 480
gtt                                                             483
```

<210> 49
<211> 1547
<212> DNA
<213> Canis familiaris

<220>
<221> CDS
<222> (1)..(1215)

<400> 49

```
ggc ggg gtc gcc gca ccc acc gaa act cag cca cct gtg acg aat ttg    48
Gly Gly Val Ala Ala Pro Thr Glu Thr Gln Pro Pro Val Thr Asn Leu
  1               5                  10                  15

agt gtt tct gtt gaa aac ctc tgc acg gtc ata tgg aca tgg aac cct    96
Ser Val Ser Val Glu Asn Leu Cys Thr Val Ile Trp Thr Trp Asn Pro
             20                  25                  30

ccc gag gga gcc agc ccg aat tgc acc tta cgg tat ttt agt cat ttt   144
Pro Glu Gly Ala Ser Pro Asn Cys Thr Leu Arg Tyr Phe Ser His Phe
         35                  40                  45

gac aac aaa cag gat aag aaa att gct cct gaa act cat cgt tca aaa   192
Asp Asn Lys Gln Asp Lys Lys Ile Ala Pro Glu Thr His Arg Ser Lys
     50                  55                  60

gaa gta ccc ctg aat gag agg att tgt ctg caa gtg ggg tcc cag tgc   240
Glu Val Pro Leu Asn Glu Arg Ile Cys Leu Gln Val Gly Ser Gln Cys
 65                  70                  75                  80

agc acc aat gaa agt gac aat cct agc att ttg gtg gaa aag tgc acc   288
Ser Thr Asn Glu Ser Asp Asn Pro Ser Ile Leu Val Glu Lys Cys Thr
                 85                  90                  95

cca cca cct gaa ggt gat cct gag tcg gct gtg act gag cta caa tgt   336
```

49

```
Pro Pro Pro Glu Gly Asp Pro Glu Ser Ala Val Thr Glu Leu Gln Cys
            100             105             110

gtt tgg cac aac ctg agc tac atg aag tgt act tgg ctt cct gga agg    384
Val Trp His Asn Leu Ser Tyr Met Lys Cys Thr Trp Leu Pro Gly Arg
        115             120             125

aat aca agc cct gac acc aac tat act ctc tac tat tgg cac agc agc    432
Asn Thr Ser Pro Asp Thr Asn Tyr Thr Leu Tyr Tyr Trp His Ser Ser
    130             135             140

ctg gga aaa att ctt caa tgc gaa gac atc tat aga gaa ggt caa cac    480
Leu Gly Lys Ile Leu Gln Cys Glu Asp Ile Tyr Arg Glu Gly Gln His
145             150             155             160

att ggt tgt tcc ttt gct ctg act aat ttg aag gat tcc agt ttt gaa    528
Ile Gly Cys Ser Phe Ala Leu Thr Asn Leu Lys Asp Ser Ser Phe Glu
                165             170             175

caa cac agt gtc caa ata atg gtc aag gat aat gca aga aaa att aga    576
Gln His Ser Val Gln Ile Met Val Lys Asp Asn Ala Arg Lys Ile Arg
            180             185             190

ccg tcc ttc aat ata gtg cct tta act tct cat gtg aaa cct gat ccc    624
Pro Ser Phe Asn Ile Val Pro Leu Thr Ser His Val Lys Pro Asp Pro
            195             200             205

ccc cat att aag cgt ctc ttc ttc caa aat ggt aac ttg tat gtg caa    672
Pro His Ile Lys Arg Leu Phe Phe Gln Asn Gly Asn Leu Tyr Val Gln
    210             215             220

tgg aag aat cca caa aat ttt tat agc aga tgc tta tct tac caa gta    720
Trp Lys Asn Pro Gln Asn Phe Tyr Ser Arg Cys Leu Ser Tyr Gln Val
225             230             235             240

gaa gtc aat aac agc cag act gag acg aat gat ata ttc tac gtt gaa    768
Glu Val Asn Asn Ser Gln Thr Glu Thr Asn Asp Ile Phe Tyr Val Glu
                245             250             255

gaa gcc aaa tgt cag aat tca gaa ttt gag gga aac ctg gag ggt aca    816
Glu Ala Lys Cys Gln Asn Ser Glu Phe Glu Gly Asn Leu Glu Gly Thr
            260             265             270

att tgt ttc atg gtc ccc ggc gtt ctt cct gat act ttg aac aca gtc    864
Ile Cys Phe Met Val Pro Gly Val Leu Pro Asp Thr Leu Asn Thr Val
            275             280             285

aga ata aga gtc aga aca aat aag tta tgc tat gag gat gac aaa ctc    912
```

50

```
Arg Ile Arg Val Arg Thr Asn Lys Leu Cys Tyr Glu Asp Asp Lys Leu
    290                 295                 300

tgg agt aat tgg agt caa gcg atg agt ata ggt gag aat acc gac ccc      960
Trp Ser Asn Trp Ser Gln Ala Met Ser Ile Gly Glu Asn Thr Asp Pro
305                 310                 315                 320

acg ttc tat ata acc atg ttg ctc gcc act caa gtc atc gtt gca ggt     1008
Thr Phe Tyr Ile Thr Met Leu Leu Ala Thr Gln Val Ile Val Ala Gly
                    325                 330                 335

gcc atc ata atc ctt ctg ctt tat ctc aaa agg ctc aag atc att ata     1056
Ala Ile Ile Ile Leu Leu Leu Tyr Leu Lys Arg Leu Lys Ile Ile Ile
            340                 345                 350

ttc cct cca att cct gat cct ggc aag att ttt aaa gaa atg ttt gga     1104
Phe Pro Pro Ile Pro Asp Pro Gly Lys Ile Phe Lys Glu Met Phe Gly
            355                 360                 365

gac cag aat gat gat acg ctg cac tgg agg aag tac gac atc tat gag     1152
Asp Gln Asn Asp Asp Thr Leu His Trp Arg Lys Tyr Asp Ile Tyr Glu
        370                 375                 380

aag caa aca aaa gaa gaa acg gac tca gta gtg ctg att gaa aac ctg     1200
Lys Gln Thr Lys Glu Glu Thr Asp Ser Val Val Leu Ile Glu Asn Leu
385                 390                 395                 400

aag aaa gcc tct cag taatggggat aacttatttt agccttcagc atgaccttgt     1255
Lys Lys Ala Ser Gln
                405

aaagattcat ccccacgttc tcgggaagct tcaaggtcaa gcatcttggg aaaggacatt 1315

acagtttcta cagcatggtg tacctgggca tctccgacta cttcttcaac acagcagggc 1375

ttgtgtacca agaggcaggg gccttaaaca tgaccatcac ggacgacatg ataccaaaga 1435

aatccaaatt ccgactgaca accgattttt tggggaccct cataccccaa gtggccgaga 1495

tgttccccaa catgacggtt caattcaacg tctgggcctc ctccccgccg ca           1547
```

<210> 50
<211> 405
<212> PRT
<213> Canis familiaris

<400> 50

```
Gly Gly Val Ala Ala Pro Thr Glu Thr Gln Pro Pro Val Thr Asn Leu
 1               5                  10                  15

Ser Val Ser Val Glu Asn Leu Cys Thr Val Ile Trp Thr Trp Asn Pro
                20                  25                  30

Pro Glu Gly Ala Ser Pro Asn Cys Thr Leu Arg Tyr Phe Ser His Phe
            35                  40                  45

Asp Asn Lys Gln Asp Lys Lys Ile Ala Pro Glu Thr His Arg Ser Lys
        50                  55                  60

Glu Val Pro Leu Asn Glu Arg Ile Cys Leu Gln Val Gly Ser Gln Cys
65                  70                  75                  80

Ser Thr Asn Glu Ser Asp Asn Pro Ser Ile Leu Val Glu Lys Cys Thr
                85                  90                  95

Pro Pro Pro Glu Gly Asp Pro Glu Ser Ala Val Thr Glu Leu Gln Cys
            100                 105                 110

Val Trp His Asn Leu Ser Tyr Met Lys Cys Thr Trp Leu Pro Gly Arg
        115                 120                 125

Asn Thr Ser Pro Asp Thr Asn Tyr Thr Leu Tyr Tyr Trp His Ser Ser
    130                 135                 140

Leu Gly Lys Ile Leu Gln Cys Glu Asp Ile Tyr Arg Glu Gly Gln His
145                 150                 155                 160

Ile Gly Cys Ser Phe Ala Leu Thr Asn Leu Lys Asp Ser Ser Phe Glu
            165                 170                 175

Gln His Ser Val Gln Ile Met Val Lys Asp Asn Ala Arg Lys Ile Arg
            180                 185                 190

Pro Ser Phe Asn Ile Val Pro Leu Thr Ser His Val Lys Pro Asp Pro
        195                 200                 205

Pro His Ile Lys Arg Leu Phe Phe Gln Asn Gly Asn Leu Tyr Val Gln
    210                 215                 220

Trp Lys Asn Pro Gln Asn Phe Tyr Ser Arg Cys Leu Ser Tyr Gln Val
225                 230                 235                 240

Glu Val Asn Asn Ser Gln Thr Glu Thr Asn Asp Ile Phe Tyr Val Glu
            245                 250                 255
```

Glu Ala Lys Cys Gln Asn Ser Glu Phe Glu Gly Asn Leu Glu Gly Thr
        260   265   270

Ile Cys Phe Met Val Pro Gly Val Leu Pro Asp Thr Leu Asn Thr Val
        275   280   285

Arg Ile Arg Val Arg Thr Asn Lys Leu Cys Tyr Glu Asp Asp Lys Leu
        290   295   300

Trp Ser Asn Trp Ser Gln Ala Met Ser Ile Gly Glu Asn Thr Asp Pro
305   310   315   320

Thr Phe Tyr Ile Thr Met Leu Leu Ala Thr Gln Val Ile Val Ala Gly
                325   330   335

Ala Ile Ile Ile Leu Leu Leu Tyr Leu Lys Arg Leu Lys Ile Ile Ile
                340   345   350

Phe Pro Pro Ile Pro Asp Pro Gly Lys Ile Phe Lys Glu Met Phe Gly
        355   360   365

Asp Gln Asn Asp Asp Thr Leu His Trp Arg Lys Tyr Asp Ile Tyr Glu
        370   375   380

Lys Gln Thr Lys Glu Glu Thr Asp Ser Val Val Leu Ile Glu Asn Leu
385   390   395   400

Lys Lys Ala Ser Gln
                405

<210> 51
<211> 1547
<212> DNA
<213> Canis familiaris

<400> 51
tgcggcgggg aggaggccca gacgttgaat tgaaccgtca tgttggggaa catctcggcc 60
acttggggta tgagggtccc caaaaaatcg gttgtcagtc ggaatttgga tttctttggt 120
atcatgtcgt ccgtgatggt catgtttaag gcccctgcct cttggtacac aagccctgct 180
gtgttgaaga agtagtcgga gatgcccagg tacaccatgc tgtagaaact gtaatgtcct 240
ttcccaagat gcttgacctt gaagcttccc gagaacgtgg ggatgaatct ttacaaggtc 300
atgctgaagg ctaaaataag ttatccccat tactgagagg ctttcttcag gttttcaatc 360
agcactactg agtccgtttc ttcttttgtt tgcttctcat agatgtcgta cttcctccag 420
tgcagcgtat catcattctg gtctccaaac atttctttaa aaatcttgcc aggatcagga 480
attggaggga atataatgat cttgagcctt ttgagataaa gcagaaggat tatgatggca 540
cctgcaacga tgacttgagt ggcgagcaac atggttatat agaacgtggg gtcggtattc 600

```
tcacctatac tcatcgcttg actccaatta ctccagagtt tgtcatcctc atagcataac 660
ttatttgttc tgactcttat tctgactgtg ttcaaagtat caggaagaac gccgggggacc 720
atgaaacaaa ttgtaccctc caggtttccc tcaaattctg aattctgaca tttggcttct 780
tcaacgtaga atatatcatt cgtctcagtc tggctgttat tgacttctac ttggtaagat 840
aagcatctgc tataaaaatt ttgtggattc ttccattgca catacaagtt accattttgg 900
aagaagagac gcttaatatg gggggggatca ggtttcacat gagaagttaa aggcactata 960
ttgaaggacg gtctaatttt tcttgcatta tccttgacca ttatttggac actgtgttgt 1020
tcaaaactgg aatccttcaa attagtcaga gcaaaggaac aaccaatgtg ttgaccttct 1080
ctatagatgt cttcgcattg aagaattttt cccaggctgc tgtgccaata gtagagagta 1140
tagttggtgt cagggcttgt attccttcca ggaagccaag tacacttcat gtagctcagg 1200
ttgtgccaaa cacattgtag ctcagtcaca gccgactcag gatcaccttc aggtggtggg 1260
gtgcactttt ccaccaaaat gctaggattg tcactttcat tggtgctgca ctgggacccc 1320
acttgcagac aaatcctctc attcagggggt acttcttttg aacgatgagt ttcaggagca 1380
attttcttat cctgtttgtt gtcaaaatga ctaaaatacc gtaaggtgca attcgggctg 1440
gctccctcgg gagggttcca tgtccatatg accgtgcaga ggttttcaac agaaacactc 1500
aaattcgtca caggtggctg agtttcggtg ggtgcggcga ccccgcc      1547
```

<210> 52
<211> 1215
<212> DNA
<213> Canis familiaris

<400> 52
```
ggcggggtcg ccgcacccac cgaaactcag ccacctgtga cgaatttgag tgtttctgtt 60
gaaaacctct gcacggtcat atggacatgg aaccctcccg agggagccag cccgaattgc 120
accttacggt attttagtca ttttgacaac aaacaggata agaaaattgc tcctgaaact 180
catcgttcaa aagaagtacc cctgaatgag aggatttgtc tgcaagtggg gtcccagtgc 240
agcaccaatg aaagtgacaa tcctagcatt ttggtggaaa agtgcacccc accacctgaa 300
ggtgatcctg agtcggctgt gactgagcta caatgtgttt ggcacaacct gagctacatg 360
aagtgtactt ggcttcctgg aaggaataca agccctgaca ccaactatac tctctactat 420
tggcacagca gcctgggaaa aattcttcaa tgcgaagaca tctatagaga aggtcaacac 480
attggttgtt cctttgctct gactaatttg aaggattcca gttttgaaca acacagtgtc 540
caaataatgg tcaaggataa tgcaagaaaa attagaccgt ccttcaatat agtgccttta 600
acttctcatg tgaaacctga tcccccccat attaagcgtc tcttcttcca aaatggtaac 660
ttgtatgtgc aatggaagaa tccacaaaat ttttatagca gatgcttatc ttaccaagta 720
gaagtcaata acagccagac tgagacgaat gatatattct acgttgaaga agccaaatgt 780
cagaattcag aatttgaggg aaacctggag ggtacaattt gtttcatggt ccccggcgtt 840
cttcctgata cttttgaacac agtcagaata agagtcagaa caaataagtt atgctatgag 900
gatgacaaac tctggagtaa ttggagtcaa gcgatgagta taggtgagaa taccgacccc 960
acgttctata taaccatgtt gctcgccact caagtcatcg ttgcaggtgc catcataatc 1020
cttctgcttt atctcaaaag gctcaagatc attatattcc ctccaattcc tgatcctggc 1080
aagatttta aagaaatgtt tggagaccag aatgatgata cgctgcactg gaggaagtac 1140
gacatctatg agaagcaaac aaaagaagaa acggactcag tagtgctgat tgaaaacctg 1200
aagaaagcct ctcag                                      1215
```

<210> 53
```

<211> 1215
<212> DNA
<213> Canis familiaris

<400> 53
ctgagaggct ttcttcaggt tttcaatcag cactactgag tccgtttctt cttttgtttg 60
cttctcatag atgtcgtact tcctccagtg cagcgtatca tcattctggt ctccaaacat 120
ttctttaaaa atcttgccag gatcaggaat tggagggaat ataatgatct tgagcctttt 180
gagataaagc agaaggatta tgatggcacc tgcaacgatg acttgagtgg cgagcaacat 240
ggttatatag aacgtggggt cggtattctc acctatactc atcgcttgac tccaattact 300
ccagagtttg tcatcctcat agcataactt atttgttctg actcttattc tgactgtgtt 360
caaagtatca ggaagaacgc cggggaccat gaaacaaatt gtaccctcca ggtttccctc 420
aaattctgaa ttctgacatt tggcttcttc aacgtagaat atatcattcg tctcagtctg 480
gctgttattg acttctactt ggtaagataa gcatctgcta taaaaatttt gtggattctt 540
ccattgcaca tacaagttac cattttggaa gaagagacgc ttaatatggg ggggatcagg 600
tttcacatga gaagttaaag gcactatatt gaaggacggt ctaatttttc ttgcattatc 660
cttgaccatt atttggacac tgtgttgttc aaaactggaa tccttcaaat tagtcagagc 720
aaaggaacaa ccaatgtgtt gaccttctct atagatgtct cgcattgaa gaattttttcc 780
caggctgctg tgccaatagt agagagtata gttggtgtca gggcttgtat tccttccagg 840
aagccaagta cacttcatgt agctcaggtt gtgccaaaca cattgtagct cagtcacagc 900
cgactcagga tcaccttcag gtggtggggt gcacttttcc accaaaatgc taggattgtc 960
actttcattg gtgctgcact gggacccccac ttgcagacaa atcctctcat tcaggggtac 1020
ttcttttgaa cgatgagttt caggagcaat tttcttatcc tgtttgttgt caaaatgact 1080
aaaataccgt aaggtgcaat tcgggctggc tccctcggga gggttccatg tccatatgac 1140
cgtgcagagg ttttcaacag aaacactcaa attcgtcaca ggtggctgag tttcggtggg 1200
tgcggcgacc ccgcc 1215


<210> 54
<211> 620
<212> DNA
<213> Canis familiaris

<220>
<221> CDS
<222> (184)..(618)

<400> 54
ggcacgaggc tgagtttgtg tgcttgatta tcagacagga agggaagtct tagagattct 60

aattaatgtc tccaaactgg agaagagaaa aaaaagagga cctgtgataa ttgcctatga 120

taattcattt cttgagaaac catattattg agtggaaact tcaaagtatt gaatcttgga 180

gga atg gct ttc att cat ttg gat gtc gga ttc ctc tat acc ctg ctt    228
    Met Ala Phe Ile His Leu Asp Val Gly Phe Leu Tyr Thr Leu Leu
    1               5                   10                  15

```
gtt tgc aca gca ttt ggc tct atg ctt tca aat gct gag ata aaa gtt      276
Val Cys Thr Ala Phe Gly Ser Met Leu Ser Asn Ala Glu Ile Lys Val
              20                  25                  30

aat cct cct cag gat ttt gag ata gtg gac cct gga tat tta ggt tat      324
Asn Pro Pro Gln Asp Phe Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr
              35                  40                  45

ctc tct ttg caa tgg caa cct cca tta ttt ccg gat aat ttt aag gaa      372
Leu Ser Leu Gln Trp Gln Pro Pro Leu Phe Pro Asp Asn Phe Lys Glu
          50                  55                  60

tgc aca ata gaa tat gaa tta aaa tac cga aac att gat agt gaa aac      420
Cys Thr Ile Glu Tyr Glu Leu Lys Tyr Arg Asn Ile Asp Ser Glu Asn
      65                  70                  75

tgg aag acc atc att acc aag aat cta cat tac aaa gat ggg ttt gat      468
Trp Lys Thr Ile Ile Thr Lys Asn Leu His Tyr Lys Asp Gly Phe Asp
  80                  85                  90                  95

ctt aac aaa ggt att gaa gca aag ata aac aca ctt ctg cca gca caa      516
Leu Asn Lys Gly Ile Glu Ala Lys Ile Asn Thr Leu Leu Pro Ala Gln
              100                 105                 110

tgc aca aat gga tca gaa gtt aga agt tca tgg gca gaa act act tat      564
Cys Thr Asn Gly Ser Glu Val Arg Ser Ser Trp Ala Glu Thr Thr Tyr
              115                 120                 125

tgg aca tca cca caa gga aat cgg gaa act aaa att caa gat atg gac      612
Trp Thr Ser Pro Gln Gly Asn Arg Glu Thr Lys Ile Gln Asp Met Asp
          130                 135                 140

tgt gta ta                                                           620
Cys Val
      145


<210> 55
<211> 145
<212> PRT
<213> Canis familiaris

<400> 55
Met Ala Phe Ile His Leu Asp Val Gly Phe Leu Tyr Thr Leu Leu Val
  1               5                   10                  15

Cys Thr Ala Phe Gly Ser Met Leu Ser Asn Ala Glu Ile Lys Val Asn
              20                  25                  30
```

56

Pro Pro Gln Asp Phe Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr Leu
        35   40   45

Ser Leu Gln Trp Gln Pro Pro Leu Phe Pro Asp Asn Phe Lys Glu Cys
        50   55   60

Thr Ile Glu Tyr Glu Leu Lys Tyr Arg Asn Ile Asp Ser Glu Asn Trp
65   70   75   80

Lys Thr Ile Ile Thr Lys Asn Leu His Tyr Lys Asp Gly Phe Asp Leu
                85   90   95

Asn Lys Gly Ile Glu Ala Lys Ile Asn Thr Leu Leu Pro Ala Gln Cys
            100   105   110

Thr Asn Gly Ser Glu Val Arg Ser Ser Trp Ala Glu Thr Thr Tyr Trp
            115   120   125

Thr Ser Pro Gln Gly Asn Arg Glu Thr Lys Ile Gln Asp Met Asp Cys
        130   135   140

Val
145

<210> 56
<211> 620
<212> DNA
<213> Canis familiaris

<400> 56
tatacacagt ccatatcttg aattttagtt tcccgatttc cttgtggtga tgtccaataa 60
gtagtttctg cccatgaact tctaacttct gatccatttg tgcattgtgc tggcagaagt 120
gtgtttatct ttgcttcaat acctttgtta agatcaaacc catctttgta atgtagattc 180
ttggtaatga tggtcttcca gttttcacta tcaatgtttc ggtattttaa ttcatattct 240
attgtgcatt ccttaaaatt atccggaaat aatggaggtt gccattgcaa agagagataa 300
cctaaatatc cagggtccac tatctcaaaa tcctgaggag gattaacttt tatctcagca 360
tttgaaagca tagagccaaa tgctgtgcaa acaagcaggg tatagaggaa tccgacatcc 420
aaatgaatga aagccattcc tccaagattc aatactttga gtttccact caataatatg 480
gtttctcaag aaatgaatta tcataggcaa ttatcacagg tcctcttttt tttctcttct 540
ccagtttgga gacattaatt agaatctcta agacttccct tcctgtctga taatcaagca 600
cacaaactca gcctcgtgcc   620

<210> 57
<211> 878

<400> 57

caa	gga	aat	cgg	gaa	act	aaa	att	caa	gat	atg	gac	tgt	gta	tat	tac	48
Gln	Gly	Asn	Arg	Glu	Thr	Lys	Ile	Gln	Asp	Met	Asp	Cys	Val	Tyr	Tyr	
1				5					10					15		

aac	tgg	caa	tat	tta	gtc	tgc	tct	tgg	aaa	cct	ggc	atg	ggt	gtc	cat	96
Asn	Trp	Gln	Tyr	Leu	Val	Cys	Ser	Trp	Lys	Pro	Gly	Met	Gly	Val	His	
		20					25					30				

ttt	gat	acc	aat	tac	cag	ttg	ttt	tac	tgg	tat	gag	ggc	ttg	gac	cat	144
Phe	Asp	Thr	Asn	Tyr	Gln	Leu	Phe	Tyr	Trp	Tyr	Glu	Gly	Leu	Asp	His	
		35					40					45				

tca	gca	gag	tgt	act	gat	tac	atc	aag	gtt	aat	gga	aaa	aat	atg	gga	192
Ser	Ala	Glu	Cys	Thr	Asp	Tyr	Ile	Lys	Val	Asn	Gly	Lys	Asn	Met	Gly	
	50					55					60					

tgc	agg	ttt	ccc	tat	ttg	gag	tca	tca	gac	tat	aaa	gat	ttc	tac	atc	240
Cys	Arg	Phe	Pro	Tyr	Leu	Glu	Ser	Ser	Asp	Tyr	Lys	Asp	Phe	Tyr	Ile	
65					70					75					80	

tgt	gtt	aat	ggg	tca	tca	gaa	tcc	cag	cct	atc	aga	ccc	agc	tat	ttt	288
Cys	Val	Asn	Gly	Ser	Ser	Glu	Ser	Gln	Pro	Ile	Arg	Pro	Ser	Tyr	Phe	
			85					90					95			

att	ttt	cag	ctt	caa	aat	ata	gtt	aaa	cct	atg	cca	cca	gac	tac	ctt	336
Ile	Phe	Gln	Leu	Gln	Asn	Ile	Val	Lys	Pro	Met	Pro	Pro	Asp	Tyr	Leu	
		100					105					110				

agt	ctt	act	gtg	aag	aat	tca	gag	gaa	att	aac	ctg	aaa	tgg	aac	atg	384
Ser	Leu	Thr	Val	Lys	Asn	Ser	Glu	Glu	Ile	Asn	Leu	Lys	Trp	Asn	Met	
		115					120					125				

cct	aaa	gga	ccc	att	cca	gcc	aaa	tgt	ttc	att	tat	gaa	att	gaa	ttc	432
Pro	Lys	Gly	Pro	Ile	Pro	Ala	Lys	Cys	Phe	Ile	Tyr	Glu	Ile	Glu	Phe	
	130					135					140					

aca	gag	gat	ggt	act	act	tgg	gtg	act	acc	aca	gtt	gag	aat	gag	ata	480

```
Thr Glu Asp Gly Thr Thr Trp Val Thr Thr Thr Val Glu Asn Glu Ile
145                 150             155                 160


caa atc aca aga aca tca aat gaa agc caa aaa tta tgc ttt ttg gta     528
Gln Ile Thr Arg Thr Ser Asn Glu Ser Gln Lys Leu Cys Phe Leu Val
                165             170                 175


aga agt aaa gtg aat att tat tgc tca gat gat gga atc tgg agt gag     576
Arg Ser Lys Val Asn Ile Tyr Cys Ser Asp Asp Gly Ile Trp Ser Glu
                180             185                 190


tgg agt gat gaa caa tgc tgg aaa ggt gac ata tgg aag gaa acc tta     624
Trp Ser Asp Glu Gln Cys Trp Lys Gly Asp Ile Trp Lys Glu Thr Leu
            195             200                 205


gta ttt ttc ttg ata cca ttt gct ttt gtc tca ata ttt gtt ttg gta     672
Val Phe Phe Leu Ile Pro Phe Ala Phe Val Ser Ile Phe Val Leu Val
            210             215                 220


ata act tgc ctg ctt ttg tat aag caa agg gct tta ctg aaa acg atc     720
Ile Thr Cys Leu Leu Leu Tyr Lys Gln Arg Ala Leu Leu Lys Thr Ile
225                 230             235                 240


ttt cat aca aaa aaa gaa gtc ttt tct cat caa gac aca ttc tgt         765
Phe His Thr Lys Lys Glu Val Phe Ser His Gln Asp Thr Phe Cys
                245             250                 255


tgactcagta actttcagtc ttatggccag atgttaaata tgagtcttat taaactgaag 825


cttttcctca aatattgaat aaatcttatt ttaaaangaa aaaaaaaaaa aaa         878



<210> 58
<211> 255
<212> PRT
<213> Canis familiaris
<223> At location 862, n = unknown

<400> 58
Gln Gly Asn Arg Glu Thr Lys Ile Gln Asp Met Asp Cys Val Tyr Tyr
 1               5                  10                  15


Asn Trp Gln Tyr Leu Val Cys Ser Trp Lys Pro Gly Met Gly Val His
                20              25                  30


Phe Asp Thr Asn Tyr Gln Leu Phe Tyr Trp Tyr Glu Gly Leu Asp His
            35              40                  45
```

Ser Ala Glu Cys Thr Asp Tyr Ile Lys Val Asn Gly Lys Asn Met Gly
    50   55   60

Cys Arg Phe Pro Tyr Leu Glu Ser Ser Asp Tyr Lys Asp Phe Tyr Ile
    65   70   75   80

Cys Val Asn Gly Ser Ser Glu Ser Gln Pro Ile Arg Pro Ser Tyr Phe
                85   90   95

Ile Phe Gln Leu Gln Asn Ile Val Lys Pro Met Pro Pro Asp Tyr Leu
            100   105   110

Ser Leu Thr Val Lys Asn Ser Glu Glu Ile Asn Leu Lys Trp Asn Met
            115   120   125

Pro Lys Gly Pro Ile Pro Ala Lys Cys Phe Ile Tyr Glu Ile Glu Phe
    130   135   140

Thr Glu Asp Gly Thr Thr Trp Val Thr Thr Thr Val Glu Asn Glu Ile
145   150   155   160

Gln Ile Thr Arg Thr Ser Asn Glu Ser Gln Lys Leu Cys Phe Leu Val
                165   170   175

Arg Ser Lys Val Asn Ile Tyr Cys Ser Asp Asp Gly Ile Trp Ser Glu
            180   185   190

Trp Ser Asp Glu Gln Cys Trp Lys Gly Asp Ile Trp Lys Glu Thr Leu
            195   200   205

Val Phe Phe Leu Ile Pro Phe Ala Phe Val Ser Ile Phe Val Leu Val
    210   215   220

Ile Thr Cys Leu Leu Leu Tyr Lys Gln Arg Ala Leu Leu Lys Thr Ile
225   230   235   240

Phe His Thr Lys Lys Glu Val Phe Ser His Gln Asp Thr Phe Cys
                245   250   255

<210> 59
<211> 878
<212> DNA
<213> Canis familiaris

<400> 59
tttttttttt tttttcnttt taaaataaga tttattcaat atttgaggaa aagcttcagt 60

ttaataagac tcatatttaa catctggcca taagactgaa agttactgag tcaacagaat 120
gtgtcttgat gagaaaagac ttcttttttt gtatgaaaga tcgttttcag taaagccctt 180
tgcttataca aaagcaggca agttattacc aaaacaaata ttgagacaaa agcaaatggt 240
atcaagaaaa atactaaggt ttccttccat atgtcacctt ccagcattg ttcatcactc 300
cactcactcc agattccatc atctgagcaa taaatattca ctttacttct taccaaaaag 360
cataattttt ggctttcatt tgatgttctt gtgatttgta tctcattctc aactgtggta 420
gtcacccaag tagtaccatc ctctgtgaat tcaatttcat aaatgaaaca tttggctgga 480
atgggtcctt taggcatgtt ccatttcagg ttaatttcct ctgaattctt cacagtaaga 540
ctaaggtagt ctggtggcat aggtttaact atattttgaa gctgaaaaat aaaatagctg 600
ggtctgatag ctgggattc tgatgaccca ttaacacaga tgtagaaatc tttatagtct 660
gatgactcca ataggggaaa cctgcatccc atattttttc cattaacctt gatgtaatca 720
gtacactctg ctgaatggtc caagccctca taccagtaaa acaactggta attggtatca 780
aaatggacac ccatgccagg tttccaagag cagactaaat attgccagtt gtaatataca 840
cagtccatat cttgaatttt agtttcccga tttccttg   878

<210> 60
<211> 1454
<212> DNA
<213> Canis familiaris

<220>
<221> CDS
<222> (184)..(1341)

<220>
<223> At location 1438, n = unknown

<400> 60
ggcacgaggc tgagtttgtg tgcttgatta tcagacagga agggaagtct tagagattct 60

aattaatgtc tccaaactgg agaagagaaa aaaaagagga cctgtgataa ttgcctatga 120

taattcattt cttgagaaac catattattg agtggaaact tcaaagtatt gaatcttgga 180

gga atg gct ttc att cat ttg gat gtc gga ttc ctc tat acc ctg ctt   228
    Met Ala Phe Ile His Leu Asp Val Gly Phe Leu Tyr Thr Leu Leu
    1   5   10   15

gtt tgc aca gca ttt ggc tct atg ctt tca aat gct gag ata aaa gtt   276
Val Cys Thr Ala Phe Gly Ser Met Leu Ser Asn Ala Glu Ile Lys Val
                20   25   30

aat cct cct cag gat ttt gag ata gtg gac cct gga tat tta ggt tat   324
Asn Pro Pro Gln Asp Phe Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr
            35   40   45

ctc tct ttg caa tgg caa cct cca tta ttt ccg gat aat ttt aag gaa   372

61

Leu Ser Leu Gln Trp Gln Pro Pro Leu Phe Pro Asp Asn Phe Lys Glu
        50   55   60

tgc aca ata gaa tat gaa tta aaa tac cga aac att gat agt gaa aac   420
Cys Thr Ile Glu Tyr Glu Leu Lys Tyr Arg Asn Ile Asp Ser Glu Asn
        65   70   75

tgg aag acc atc att acc aag aat cta cat tac aaa gat ggg ttt gat   468
Trp Lys Thr Ile Ile Thr Lys Asn Leu His Tyr Lys Asp Gly Phe Asp
 80   85   90   95

ctt aac aaa ggt att gaa gca aag ata aac aca ctt ctg cca gca caa   516
Leu Asn Lys Gly Ile Glu Ala Lys Ile Asn Thr Leu Leu Pro Ala Gln
                100   105   110

tgc aca aat gga tca gaa gtt aga agt tca tgg gca gaa act act tat   564
Cys Thr Asn Gly Ser Glu Val Arg Ser Ser Trp Ala Glu Thr Thr Tyr
                115   120   125

tgg aca tca cca caa gga aat cgg gaa act aaa att caa gat atg gac   612
Trp Thr Ser Pro Gln Gly Asn Arg Glu Thr Lys Ile Gln Asp Met Asp
                130   135   140

tgt gta tat tac aac tgg caa tat tta gtc tgc tct tgg aaa cct ggc   660
Cys Val Tyr Tyr Asn Trp Gln Tyr Leu Val Cys Ser Trp Lys Pro Gly
                145   150   155

atg ggt gtc cat ttt gat acc aat tac cag ttg ttt tac tgg tat gag   708
Met Gly Val His Phe Asp Thr Asn Tyr Gln Leu Phe Tyr Trp Tyr Glu
160   165   170   175

ggc ttg gac cat tca gca gag tgt act gat tac atc aag gtt aat gga   756
Gly Leu Asp His Ser Ala Glu Cys Thr Asp Tyr Ile Lys Val Asn Gly
                180   185   190

aaa aat atg gga tgc agg ttt ccc tat ttg gag tca tca gac tat aaa   804
Lys Asn Met Gly Cys Arg Phe Pro Tyr Leu Glu Ser Ser Asp Tyr Lys
                195   200   205

gat ttc tac atc tgt gtt aat ggg tca tca gaa tcc cag cct atc aga   852
Asp Phe Tyr Ile Cys Val Asn Gly Ser Ser Glu Ser Gln Pro Ile Arg
                210   215   220

ccc agc tat ttt att ttt cag ctt caa aat ata gtt aaa cct atg cca   900
Pro Ser Tyr Phe Ile Phe Gln Leu Gln Asn Ile Val Lys Pro Met Pro
        225   230   235

cca gac tac ctt agt ctt act gtg aag aat tca gag gaa att aac ctg   948

62

```
Pro Asp Tyr Leu Ser Leu Thr Val Lys Asn Ser Glu Glu Ile Asn Leu
240             245             250             255

aaa tgg aac atg cct aaa gga ccc att cca gcc aaa tgt ttc att tat    996
Lys Trp Asn Met Pro Lys Gly Pro Ile Pro Ala Lys Cys Phe Ile Tyr
                260             265             270

gaa att gaa ttc aca gag gat ggt act act tgg gtg act acc aca gtt    1044
Glu Ile Glu Phe Thr Glu Asp Gly Thr Thr Trp Val Thr Thr Thr Val
                275             280             285

gag aat gag ata caa atc aca aga aca tca aat gaa agc caa aaa tta    1092
Glu Asn Glu Ile Gln Ile Thr Arg Thr Ser Asn Glu Ser Gln Lys Leu
            290             295             300

tgc ttt ttg gta aga agt aaa gtg aat att tat tgc tca gat gat gga    1140
Cys Phe Leu Val Arg Ser Lys Val Asn Ile Tyr Cys Ser Asp Asp Gly
        305             310             315

atc tgg agt gag tgg agt gat gaa caa tgc tgg aaa ggt gac ata tgg    1188
Ile Trp Ser Glu Trp Ser Asp Glu Gln Cys Trp Lys Gly Asp Ile Trp
320             325             330             335

aag gaa acc tta gta ttt ttc ttg ata cca ttt gct ttt gtc tca ata    1236
Lys Glu Thr Leu Val Phe Phe Leu Ile Pro Phe Ala Phe Val Ser Ile
                340             345             350

ttt gtt ttg gta ata act tgc ctg ctt ttg tat aag caa agg gct tta    1284
Phe Val Leu Val Ile Thr Cys Leu Leu Leu Tyr Lys Gln Arg Ala Leu
            355             360             365

ctg aaa acg atc ttt cat aca aaa aaa gaa gtc ttt tct cat caa gac    1332
Leu Lys Thr Ile Phe His Thr Lys Lys Glu Val Phe Ser His Gln Asp
        370             375             380

aca ttc tgt tgactcagta actttcagtc ttatggccag atgttaaata            1381
Thr Phe Cys
        385

tgagtcttat taaactgaag cttttcctca atattgaat aaatcttatt ttaaaangaa 1441

aaaaaaaaaa aaa                                                     1454


<210> 61
<211> 386
<212> PRT
<213> Canis familiaris
```

63

<223> At location 1438, n = unknown

<400> 61
```
Met Ala Phe Ile His Leu Asp Val Gly Phe Leu Tyr Thr Leu Leu Val
 1               5                  10                  15

Cys Thr Ala Phe Gly Ser Met Leu Ser Asn Ala Glu Ile Lys Val Asn
            20                  25                  30

Pro Pro Gln Asp Phe Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr Leu
            35                  40                  45

Ser Leu Gln Trp Gln Pro Pro Leu Phe Pro Asp Asn Phe Lys Glu Cys
        50                  55                  60

Thr Ile Glu Tyr Glu Leu Lys Tyr Arg Asn Ile Asp Ser Glu Asn Trp
65                  70                  75                  80

Lys Thr Ile Ile Thr Lys Asn Leu His Tyr Lys Asp Gly Phe Asp Leu
                85                  90                  95

Asn Lys Gly Ile Glu Ala Lys Ile Asn Thr Leu Leu Pro Ala Gln Cys
            100                 105                 110

Thr Asn Gly Ser Glu Val Arg Ser Ser Trp Ala Glu Thr Thr Tyr Trp
            115                 120                 125

Thr Ser Pro Gln Gly Asn Arg Glu Thr Lys Ile Gln Asp Met Asp Cys
        130                 135                 140

Val Tyr Tyr Asn Trp Gln Tyr Leu Val Cys Ser Trp Lys Pro Gly Met
145                 150                 155                 160

Gly Val His Phe Asp Thr Asn Tyr Gln Leu Phe Tyr Trp Tyr Glu Gly
            165                 170                 175

Leu Asp His Ser Ala Glu Cys Thr Asp Tyr Ile Lys Val Asn Gly Lys
            180                 185                 190

Asn Met Gly Cys Arg Phe Pro Tyr Leu Glu Ser Ser Asp Tyr Lys Asp
            195                 200                 205

Phe Tyr Ile Cys Val Asn Gly Ser Ser Glu Ser Gln Pro Ile Arg Pro
        210                 215                 220

Ser Tyr Phe Ile Phe Gln Leu Gln Asn Ile Val Lys Pro Met Pro Pro
225                 230                 235                 240
```

64

Asp Tyr Leu Ser Leu Thr Val Lys Asn Ser Glu Glu Ile Asn Leu Lys
            245   250   255

Trp Asn Met Pro Lys Gly Pro Ile Pro Ala Lys Cys Phe Ile Tyr Glu
            260   265   270

Ile Glu Phe Thr Glu Asp Gly Thr Thr Trp Val Thr Thr Thr Val Glu
            275   280   285

Asn Glu Ile Gln Ile Thr Arg Thr Ser Asn Glu Ser Gln Lys Leu Cys
        290   295   300

Phe Leu Val Arg Ser Lys Val Asn Ile Tyr Cys Ser Asp Asp Gly Ile
305   310   315   320

Trp Ser Glu Trp Ser Asp Glu Gln Cys Trp Lys Gly Asp Ile Trp Lys
            325   330   335

Glu Thr Leu Val Phe Phe Leu Ile Pro Phe Ala Phe Val Ser Ile Phe
            340   345   350

Val Leu Val Ile Thr Cys Leu Leu Leu Tyr Lys Gln Arg Ala Leu Leu
        355   360   365

Lys Thr Ile Phe His Thr Lys Lys Glu Val Phe Ser His Gln Asp Thr
        370   375   380

Phe Cys
385

<210> 62
<211> 1454
<212> DNA
<213> Canis familiaris

<220>
<223> At location 17, n = unknown

<400> 62
tttttttttt tttttcnttt taaaataaga tttattcaat atttgaggaa aagcttcagt 60
ttaataagac tcatatttaa catctggcca taagactgaa agttactgag tcaacagaat 120
gtgtcttgat gagaaaagac ttcttttttt gtatgaaaga tcgttttcag taaagccctt 180
tgcttataca aaagcaggca agttattacc aaaacaaata ttgagacaaa agcaaatggt 240
atcaagaaaa atactaaggt ttccttccat atgtcacctt ccagcattg ttcatcactc 300
cactcactcc agattccatc atctgagcaa taaatattca ctttacttct taccaaaaag 360
cataattttt ggctttcatt tgatgttctt gtgatttgta tctcattctc aactgtggta 420

```
gtcacccaag tagtaccatc ctctgtgaat tcaatttcat aaatgaaaca tttggctgga 480
atgggtcctt taggcatgtt ccatttcagg ttaatttcct ctgaattctt cacagtaaga 540
ctaaggtagt ctggtggcat aggtttaact atattttgaa gctgaaaaat aaaatagctg 600
ggtctgatag gctgggattc tgatgaccca ttaacacaga tgtagaaatc tttatagtct 660
gatgactcca aataggaaaa cctgcatccc atattttttc cattaacctt gatgtaatca 720
gtacactctg ctgaatggtc caagccctca taccagtaaa acaactggta attggtatca 780
aaatggacac ccatgccagg tttccaagag cagactaaat attgccagtt gtaatataca 840
cagtccatat cttgaatttt agtttcccga tttccttgtg gtgatgtcca ataagtagtt 900
tctgcccatg aacttctaac ttctgatcca tttgtgcatt gtgctggcag aagtgtgttt 960
atctttgctt caataccttt gttaagatca aacccatctt tgtaatgtag attcttggta 1020
atgatggtct tccagttttc actatcaatg tttcggtatt ttaattcata ttctattgtg 1080
cattccttaa aattatccgg aaataatgga ggttgccatt gcaaagagag ataacctaaa 1140
tatccagggt ccactatctc aaaatcctga ggaggattaa cttttatctc agcatttgaa 1200
agcatagagc caaatgctgt gcaaacaagc agggtataga ggaatccgac atccaaatga 1260
atgaaagcca ttcctccaag attcaatact ttgaagtttc cactcaataa tatggtttct 1320
caagaaatga attatcatag gcaattatca caggtcctct tttttttctc ttctccagtt 1380
tggagacatt aattagaatc tctaagactt cccttcctgt ctgataatca agcacacaaa 1440
ctcagcctcg tgcc                                                   1454


<210> 63
<211> 1158
<212> DNA
<213> Canis familiaris

<400> 63
atggctttca ttcatttgga tgtcggattc ctctataccc tgcttgtttg cacagcattt 60
ggctctatgc tttcaaatgc tgagataaaa gttaatcctc ctcaggattt tgagatagtg 120
gaccctggat atttaggtta tctctctttg caatggcaac ctccattatt tccggataat 180
tttaaggaat gcacaataga atatgaatta aaataccgaa acattgatag tgaaaactgg 240
aagaccatca ttaccaagaa tctacattac aaagatgggt ttgatcttaa caaaggtatt 300
gaagcaaaga taaacacact tctgccagca caatgcacaa atggatcaga agttagaagt 360
tcatgggcag aaactactta ttggacatca ccacaaggaa atcgggaaac taaaattcaa 420
gatatggact gtgtatatta caactggcaa tatttagtct gctcttggaa acctggcatg 480
ggtgtccatt ttgataccaa ttaccagttg ttttactggt atgagggctt ggaccattca 540
gcagagtgta ctgattacat caaggttaat ggaaaaaata tgggatgcag gtttccctat 600
ttggagtcat cagactataa agatttctac atctgtgtta atgggtcatc agaatcccag 660
cctatcagac ccagctattt tattttttcag cttcaaaata tagttaaacc tatgccacca 720
gactacctta gtcttactgt gaagaattca gaggaaatta acctgaaatg gaacatgcct 780
aaaggaccca ttccagccaa atgtttcatt tatgaaattg aattcacaga ggatggtact 840
acttgggtga ctaccacagt tgagaatgag atacaaatca caagaacatc aaatgaaagc 900
caaaaattat gcttttggt aagaagtaaa gtgaatattt attgctcaga tgatggaatc 960
tggagtgagt ggagtgatga caatgctggg aaaggtgaca tatggaagga aaccttagta 1020
tttttcttga taccatttgc ttttgtctca atatttgttt ggtaataac ttgcctgctt 1080
ttgtataagc aaagggcttt actgaaaacg atctttcata caaaaaaaga agtctttct 1140
catcaagaca cattctgt                                              1158
```

<210> 64
<211> 1158
<212> DNA
<213> Canis familiaris

<400> 64
acagaatgtg tcttgatgag aaaagacttc ttttttttgta tgaaagatcg ttttcagtaa 60
agcccttttgc ttatacaaaa gcaggcaagt tattaccaaa acaaatattg agacaaaagc 120
aaatggtatc aagaaaaata ctaaggtttc cttccatatg tcacctttcc agcattgttc 180
atcactccac tcactccaga ttccatcatc tgagcaataa atattcactt tacttcttac 240
caaaaagcat aattttttggc tttcatttga tgttcttgtg atttgtatct cattctcaac 300
tgtggtagtc acccaagtag taccatcctc tgtgaattca atttcataaa tgaaacattt 360
ggctggaatg ggtcctttag gcatgttcca tttcaggtta atttcctctg aattcttcac 420
agtaagacta aggtagtctg gtggcatagg tttaactata ttttgaagct gaaaaataaa 480
atagctgggt ctgataggct gggattctga tgacccatta acacagatgt agaaatcttt 540
atagtctgat gactccaaat agggaaacct gcatcccata tttttttccat taaccttgat 600
gtaatcagta cactctgctg aatggtccaa gccctcatac cagtaaaaca actggtaatt 660
ggtatcaaaa tggacaccca tgccaggttt ccaagagcag actaaatatt gccagttgta 720
atatacacag tccatatctt gaattttagt ttcccgattt ccttgtggtg atgtccaata 780
agtagtttct gcccatgaac ttctaacttc tgatccattt gtgcattgtg ctggcagaag 840
tgtgtttatc tttgcttcaa tacctttgtt aagatcaaac ccatctttgt aatgtagatt 900
cttggtaatg atggtcttcc agttttcact atcaatgttt cggtatttta attcatattc 960
tattgtgcat tccttaaaat tatccggaaa taatggaggt tgccattgca aagagagata 1020
acctaaatat ccagggtcca ctatctcaaa atcctgagga ggattaactt ttatctcagc 1080
atttgaaagc atagagccaa atgctgtgca aacaagcagg gtatagagga atccgacatc 1140
caaatgaatg aaagccat 1158

<210> 65
<211> 1095
<212> DNA
<213> Canis familiaris

<220>
<221> CDS
<222> (1)..(1095)

<400> 65
tct atg ctt tca aat gct gag ata aaa gtt aat cct cct cag gat ttt   48
Ser Met Leu Ser Asn Ala Glu Ile Lys Val Asn Pro Pro Gln Asp Phe
  1   5   10   15

gag ata gtg gac cct gga tat tta ggt tat ctc tct ttg caa tgg caa   96
Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr Leu Ser Leu Gln Trp Gln
                20   25   30

cct cca tta ttt ccg gat aat ttt aag gaa tgc aca ata gaa tat gaa   144
Pro Pro Leu Phe Pro Asp Asn Phe Lys Glu Cys Thr Ile Glu Tyr Glu

tta aaa tac cga aac att gat agt gaa aac tgg aag acc atc att acc   192
Leu Lys Tyr Arg Asn Ile Asp Ser Glu Asn Trp Lys Thr Ile Ile Thr
        50   55   60

aag aat cta cat tac aaa gat ggg ttt gat ctt aac aaa ggt att gaa   240
Lys Asn Leu His Tyr Lys Asp Gly Phe Asp Leu Asn Lys Gly Ile Glu
    65   70   75   80

gca aag ata aac aca ctt ctg cca gca caa tgc aca aat gga tca gaa   288
Ala Lys Ile Asn Thr Leu Leu Pro Ala Gln Cys Thr Asn Gly Ser Glu
                85   90   95

gtt aga agt tca tgg gca gaa act act tat tgg aca tca cca caa gga   336
Val Arg Ser Ser Trp Ala Glu Thr Thr Tyr Trp Thr Ser Pro Gln Gly
                100   105   110

aat cgg gaa act aaa att caa gat atg gac tgt gta tat tac aac tgg   384
Asn Arg Glu Thr Lys Ile Gln Asp Met Asp Cys Val Tyr Tyr Asn Trp
            115   120   125

caa tat tta gtc tgc tct tgg aaa cct ggc atg ggt gtc cat ttt gat   432
Gln Tyr Leu Val Cys Ser Trp Lys Pro Gly Met Gly Val His Phe Asp
        130   135   140

acc aat tac cag ttg ttt tac tgg tat gag ggc ttg gac cat tca gca   480
Thr Asn Tyr Gln Leu Phe Tyr Trp Tyr Glu Gly Leu Asp His Ser Ala
145   150   155   160

gag tgt act gat tac atc aag gtt aat gga aaa aat atg gga tgc agg   528
Glu Cys Thr Asp Tyr Ile Lys Val Asn Gly Lys Asn Met Gly Cys Arg
                165   170   175

ttt ccc tat ttg gag tca tca gac tat aaa gat ttc tac atc tgt gtt   576
Phe Pro Tyr Leu Glu Ser Ser Asp Tyr Lys Asp Phe Tyr Ile Cys Val
                180   185   190

aat ggg tca tca gaa tcc cag cct atc aga ccc agc tat ttt att ttt   624
Asn Gly Ser Ser Glu Ser Gln Pro Ile Arg Pro Ser Tyr Phe Ile Phe
            195   200   205

cag ctt caa aat ata gtt aaa cct atg cca cca gac tac ctt agt ctt   672
Gln Leu Gln Asn Ile Val Lys Pro Met Pro Pro Asp Tyr Leu Ser Leu
        210   215   220

act gtg aag aat tca gag gaa att aac ctg aaa tgg aac atg cct aaa   720
Thr Val Lys Asn Ser Glu Glu Ile Asn Leu Lys Trp Asn Met Pro Lys

```
gga ccc att cca gcc aaa tgt ttc att tat gaa att gaa ttc aca gag    768
Gly Pro Ile Pro Ala Lys Cys Phe Ile Tyr Glu Ile Glu Phe Thr Glu
            245                 250                 255

gat ggt act act tgg gtg act acc aca gtt gag aat gag ata caa atc    816
Asp Gly Thr Thr Trp Val Thr Thr Thr Val Glu Asn Glu Ile Gln Ile
            260                 265                 270

aca aga aca tca aat gaa agc caa aaa tta tgc ttt ttg gta aga agt    864
Thr Arg Thr Ser Asn Glu Ser Gln Lys Leu Cys Phe Leu Val Arg Ser
            275                 280                 285

aaa gtg aat att tat tgc tca gat gat gga atc tgg agt gag tgg agt    912
Lys Val Asn Ile Tyr Cys Ser Asp Asp Gly Ile Trp Ser Glu Trp Ser
            290                 295                 300

gat gaa caa tgc tgg aaa ggt gac ata tgg aag gaa acc tta gta ttt    960
Asp Glu Gln Cys Trp Lys Gly Asp Ile Trp Lys Glu Thr Leu Val Phe
305                 310                 315                 320

ttc ttg ata cca ttt gct ttt gtc tca ata ttt gtt ttg gta ata act   1008
Phe Leu Ile Pro Phe Ala Phe Val Ser Ile Phe Val Leu Val Ile Thr
            325                 330                 335

tgc ctg ctt ttg tat aag caa agg gct tta ctg aaa acg atc ttt cat   1056
Cys Leu Leu Leu Tyr Lys Gln Arg Ala Leu Leu Lys Thr Ile Phe His
            340                 345                 350

aca aaa aaa gaa gtc ttt tct cat caa gac aca ttc tgt             1095
Thr Lys Lys Glu Val Phe Ser His Gln Asp Thr Phe Cys
            355                 360                 365


<210> 66
<211> 365
<212> PRT
<213> Canis familiaris

<400> 66
Ser Met Leu Ser Asn Ala Glu Ile Lys Val Asn Pro Pro Gln Asp Phe
  1               5                  10                  15

Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr Leu Ser Leu Gln Trp Gln
            20                  25                  30

Pro Pro Leu Phe Pro Asp Asn Phe Lys Glu Cys Thr Ile Glu Tyr Glu
```

Leu Lys Tyr Arg Asn Ile Asp Ser Glu Asn Trp Lys Thr Ile Ile Thr
    50   55   60

Lys Asn Leu His Tyr Lys Asp Gly Phe Asp Leu Asn Lys Gly Ile Glu
65   70   75   80

Ala Lys Ile Asn Thr Leu Leu Pro Ala Gln Cys Thr Asn Gly Ser Glu
                85   90   95

Val Arg Ser Ser Trp Ala Glu Thr Thr Tyr Trp Thr Ser Pro Gln Gly
            100   105   110

Asn Arg Glu Thr Lys Ile Gln Asp Met Asp Cys Val Tyr Tyr Asn Trp
            115   120   125

Gln Tyr Leu Val Cys Ser Trp Lys Pro Gly Met Gly Val His Phe Asp
    130   135   140

Thr Asn Tyr Gln Leu Phe Tyr Trp Tyr Glu Gly Leu Asp His Ser Ala
145   150   155   160

Glu Cys Thr Asp Tyr Ile Lys Val Asn Gly Lys Asn Met Gly Cys Arg
                165   170   175

Phe Pro Tyr Leu Glu Ser Ser Asp Tyr Lys Asp Phe Tyr Ile Cys Val
            180   185   190

Asn Gly Ser Ser Glu Ser Gln Pro Ile Arg Pro Ser Tyr Phe Ile Phe
            195   200   205

Gln Leu Gln Asn Ile Val Lys Pro Met Pro Pro Asp Tyr Leu Ser Leu
    210   215   220

Thr Val Lys Asn Ser Glu Glu Ile Asn Leu Lys Trp Asn Met Pro Lys
225   230   235   240

Gly Pro Ile Pro Ala Lys Cys Phe Ile Tyr Glu Ile Glu Phe Thr Glu
                245   250   255

Asp Gly Thr Thr Trp Val Thr Thr Thr Val Glu Asn Glu Ile Gln Ile
            260   265   270

Thr Arg Thr Ser Asn Glu Ser Gln Lys Leu Cys Phe Leu Val Arg Ser
            275   280   285

Lys Val Asn Ile Tyr Cys Ser Asp Asp Gly Ile Trp Ser Glu Trp Ser

70

290   295   300

Asp Glu Gln Cys Trp Lys Gly Asp Ile Trp Lys Glu Thr Leu Val Phe
305   310   315   320

Phe Leu Ile Pro Phe Ala Phe Val Ser Ile Phe Val Leu Val Ile Thr
                325   330   335

Cys Leu Leu Leu Tyr Lys Gln Arg Ala Leu Leu Lys Thr Ile Phe His
                340   345   350

Thr Lys Lys Glu Val Phe Ser His Gln Asp Thr Phe Cys
                355   360   365

<210> 67
<211> 1095
<212> DNA
<213> Canis familiaris

<400> 67
acagaatgtg tcttgatgag aaaagacttc tttttttgta tgaaagatcg ttttcagtaa 60
agccctttgc ttatacaaaa gcaggcaagt tattaccaaa acaaatattg agacaaaagc 120
aaatggtatc aagaaaaata ctaaggtttc cttccatatg tcacctttcc agcattgttc 180
atcactccac tcactccaga ttccatcatc tgagcaataa atattcactt tacttcttac 240
caaaaagcat aattttttggc tttcatttga tgttcttgtg atttgtatct cattctcaac 300
tgtggtagtc acccaagtag taccatcctc tgtgaattca atttcataaa tgaaacattt 360
ggctggaatg ggtcctttag gcatgttcca tttcaggtta atttcctctg aattcttcac 420
agtaagacta aggtagtctg gtggcatagg tttaactata ttttgaagct gaaaaataaa 480
atagctgggt ctgataggct gggattctga tgacccatta acacagatgt agaaatcttt 540
atagtctgat gactccaaat agggaaacct gcatcccata ttttttccat taaccttgat 600
gtaatcagta cactctgctg aatggtccaa gccctcatac cagtaaaaca actggtaatt 660
ggtatcaaaa tggacaccca tgccaggttt ccaagagcag actaaatatt gccagttgta 720
atatacacag tccatatctt gaattttagt ttcccgattt ccttgtggtg atgtccaata 780
agtagtttct gcccatgaac ttctaacttc tgatccattt gtgcattgtg ctggcagaag 840
tgtgtttatc tttgcttcaa tacctttgtt aagatcaaac ccatctttgt aatgtagatt 900
cttggtaatg atggtcttcc agtttcact atcaatgttt cggtatttta attcatattc 960
tattgtgcat tccttaaaat tatccggaaa taatggaggt tgccattgca aagagagata 1020
acctaaatat ccagggtcca ctatctcaaa atcctgagga ggattaactt ttatctcagc 1080
atttgaaagc ataga   1095

<210> 68
<211> 954
<212> DNA
<213> Canis familiaris

                                       71

<220>
<221> CDS
<222> (1)..(954)

<400> 68

atg	tct	atg	ctt	tca	aat	gct	gag	ata	aaa	gtt	aat	cct	cct	cag	gat	48
Met	Ser	Met	Leu	Ser	Asn	Ala	Glu	Ile	Lys	Val	Asn	Pro	Pro	Gln	Asp	
1				5					10					15		

ttt	gag	ata	gtg	gac	cct	gga	tat	tta	ggt	tat	ctc	tct	ttg	caa	tgg	96
Phe	Glu	Ile	Val	Asp	Pro	Gly	Tyr	Leu	Gly	Tyr	Leu	Ser	Leu	Gln	Trp	
			20					25					30			

caa	cct	cca	tta	ttt	ccg	gat	aat	ttt	aag	gaa	tgc	aca	ata	gaa	tat	144
Gln	Pro	Pro	Leu	Phe	Pro	Asp	Asn	Phe	Lys	Glu	Cys	Thr	Ile	Glu	Tyr	
		35					40					45				

gaa	tta	aaa	tac	cga	aac	att	gat	agt	gaa	aac	tgg	aag	acc	atc	att	192
Glu	Leu	Lys	Tyr	Arg	Asn	Ile	Asp	Ser	Glu	Asn	Trp	Lys	Thr	Ile	Ile	
	50					55					60					

acc	aag	aat	cta	cat	tac	aaa	gat	ggg	ttt	gat	ctt	aac	aaa	ggt	att	240
Thr	Lys	Asn	Leu	His	Tyr	Lys	Asp	Gly	Phe	Asp	Leu	Asn	Lys	Gly	Ile	
65					70					75					80	

gaa	gca	aag	ata	aac	aca	ctt	ctg	cca	gca	caa	tgc	aca	aat	gga	tca	288
Glu	Ala	Lys	Ile	Asn	Thr	Leu	Leu	Pro	Ala	Gln	Cys	Thr	Asn	Gly	Ser	
				85					90					95		

gaa	gtt	aga	agt	tca	tgg	gca	gaa	act	act	tat	tgg	aca	tca	cca	caa	336
Glu	Val	Arg	Ser	Ser	Trp	Ala	Glu	Thr	Thr	Tyr	Trp	Thr	Ser	Pro	Gln	
			100					105					110			

gga	aat	cgg	gaa	act	aaa	att	caa	gat	atg	gac	tgt	gta	tat	tac	aac	384
Gly	Asn	Arg	Glu	Thr	Lys	Ile	Gln	Asp	Met	Asp	Cys	Val	Tyr	Tyr	Asn	
		115					120					125				

tgg	caa	tat	tta	gtc	tgc	tct	tgg	aaa	cct	ggc	atg	ggt	gtc	cat	ttt	432
Trp	Gln	Tyr	Leu	Val	Cys	Ser	Trp	Lys	Pro	Gly	Met	Gly	Val	His	Phe	
	130					135					140					

gat	acc	aat	tac	cag	ttg	ttt	tac	tgg	tat	gag	ggc	ttg	gac	cat	tca	480
Asp	Thr	Asn	Tyr	Gln	Leu	Phe	Tyr	Trp	Tyr	Glu	Gly	Leu	Asp	His	Ser	
145					150					155					160	

gca	gag	tgt	act	gat	tac	atc	aag	gtt	aat	gga	aaa	aat	atg	gga	tgc	528
Ala	Glu	Cys	Thr	Asp	Tyr	Ile	Lys	Val	Asn	Gly	Lys	Asn	Met	Gly	Cys	
			165					170					175			

```
agg ttt ccc tat ttg gag tca tca gac tat aaa gat ttc tac atc tgt    576
Arg Phe Pro Tyr Leu Glu Ser Ser Asp Tyr Lys Asp Phe Tyr Ile Cys
            180                 185                 190

gtt aat ggg tca tca gaa tcc cag cct atc aga ccc agc tat ttt att    624
Val Asn Gly Ser Ser Glu Ser Gln Pro Ile Arg Pro Ser Tyr Phe Ile
        195                 200                 205

ttt cag ctt caa aat ata gtt aaa cct atg cca cca gac tac ctt agt    672
Phe Gln Leu Gln Asn Ile Val Lys Pro Met Pro Pro Asp Tyr Leu Ser
    210                 215                 220

ctt act gtg aag aat tca gag gaa att aac ctg aaa tgg aac atg cct    720
Leu Thr Val Lys Asn Ser Glu Glu Ile Asn Leu Lys Trp Asn Met Pro
225                 230                 235                 240

aaa gga ccc att cca gcc aaa tgt ttc att tat gaa att gaa ttc aca    768
Lys Gly Pro Ile Pro Ala Lys Cys Phe Ile Tyr Glu Ile Glu Phe Thr
                245                 250                 255

gag gat ggt act act tgg gtg act acc aca gtt gag aat gag ata caa    816
Glu Asp Gly Thr Thr Trp Val Thr Thr Thr Val Glu Asn Glu Ile Gln
            260                 265                 270

atc aca aga aca tca aat gaa agc caa aaa tta tgc ttt ttg gta aga    864
Ile Thr Arg Thr Ser Asn Glu Ser Gln Lys Leu Cys Phe Leu Val Arg
            275                 280                 285

agt aaa gtg aat att tat tgc tca gat gat gga atc tgg agt gag tgg    912
Ser Lys Val Asn Ile Tyr Cys Ser Asp Asp Gly Ile Trp Ser Glu Trp
    290                 295                 300

agt gat gaa caa tgc tgg aaa ggt gat atc tgg aag gaa acc            954
Ser Asp Glu Gln Cys Trp Lys Gly Asp Ile Trp Lys Glu Thr
305                 310                 315


<210> 69
<211> 318
<212> PRT
<213> Canis familiaris

<400> 69
Met Ser Met Leu Ser Asn Ala Glu Ile Lys Val Asn Pro Pro Gln Asp
 1               5                   10                  15

Phe Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr Leu Ser Leu Gln Trp
```

73

```
                20                        25                        30

Gln Pro Pro Leu Phe Pro Asp Asn Phe Lys Glu Cys Thr Ile Glu Tyr
         35                   40                   45

Glu Leu Lys Tyr Arg Asn Ile Asp Ser Glu Asn Trp Lys Thr Ile Ile
    50                   55                   60

Thr Lys Asn Leu His Tyr Lys Asp Gly Phe Asp Leu Asn Lys Gly Ile
65                   70                   75                   80

Glu Ala Lys Ile Asn Thr Leu Leu Pro Ala Gln Cys Thr Asn Gly Ser
             85                   90                   95

Glu Val Arg Ser Ser Trp Ala Glu Thr Thr Tyr Trp Thr Ser Pro Gln
         100                  105                  110

Gly Asn Arg Glu Thr Lys Ile Gln Asp Met Asp Cys Val Tyr Tyr Asn
         115                  120                  125

Trp Gln Tyr Leu Val Cys Ser Trp Lys Pro Gly Met Gly Val His Phe
    130                  135                  140

Asp Thr Asn Tyr Gln Leu Phe Tyr Trp Tyr Glu Gly Leu Asp His Ser
145                  150                  155                  160

Ala Glu Cys Thr Asp Tyr Ile Lys Val Asn Gly Lys Asn Met Gly Cys
             165                  170                  175

Arg Phe Pro Tyr Leu Glu Ser Ser Asp Tyr Lys Asp Phe Tyr Ile Cys
         180                  185                  190

Val Asn Gly Ser Ser Glu Ser Gln Pro Ile Arg Pro Ser Tyr Phe Ile
         195                  200                  205

Phe Gln Leu Gln Asn Ile Val Lys Pro Met Pro Pro Asp Tyr Leu Ser
    210                  215                  220

Leu Thr Val Lys Asn Ser Glu Glu Ile Asn Leu Lys Trp Asn Met Pro
225                  230                  235                  240

Lys Gly Pro Ile Pro Ala Lys Cys Phe Ile Tyr Glu Ile Glu Phe Thr
             245                  250                  255

Glu Asp Gly Thr Thr Trp Val Thr Thr Val Glu Asn Glu Ile Gln
         260                  265                  270

Ile Thr Arg Thr Ser Asn Glu Ser Gln Lys Leu Cys Phe Leu Val Arg
```

74

```
                275                   280                   285
    Ser Lys Val Asn Ile Tyr Cys Ser Asp Asp Gly Ile Trp Ser Glu Trp
        290                   295                   300


    Ser Asp Glu Gln Cys Trp Lys Gly Asp Ile Trp Lys Glu Thr
    305                   310                   315
```

<210> 70
<211> 954
<212> DNA
<213> Canis familiaris

<400> 70
```
ggtttccttc cagatatcac ctttccagca ttgttcatca ctccactcac tccagattcc 60
atcatctgag caataaatat tcactttact tcttaccaaa aagcataatt tttggctttc 120
atttgatgtt cttgtgattt gtatctcatt ctcaactgtg gtagtcaccc aagtagtacc 180
atcctctgtg aattcaattt cataaatgaa acatttggct ggaatgggtc ctttaggcat 240
gttccatttc aggttaattt cctctgaatt cttcacagta agactaaggt agtctggtgg 300
cataggttta actatatttt gaagctgaaa aataaaatag ctgggtctga taggctggga 360
ttctgatgac ccattaacac agatgtagaa atctttatag tctgatgact ccaaataggg 420
aaacctgcat cccatatttt ttccattaac cttgatgtaa tcagtacact ctgctgaatg 480
gtccaagccc tcataccagt aaaacaactg gtaattggta tcaaaatgga cacccatgcc 540
aggtttccaa gagcagacta atattgcca gttgtaatat acacagtcca tatcttgaat 600
tttagtttcc cgatttcctt gtggtgatgt ccaataagta gtttctgccc atgaacttct 660
aacttctgat ccatttgtgc attgtgctgg cagaagtgtg tttatctttg cttcaatacc 720
tttgttaaga tcaaacccat ctttgtaatg tagattcttg gtaatgatgg tcttccagtt 780
ttcactatca atgtttcggt attttaattc atattctatt gtgcattcct taaaattatc 840
cggaaataat ggaggttgcc attgcaaaga gagataacct aaatatccag ggtccactat 900
ctcaaaatcc tgaggaggat taactttat ctcagcattt gaaagcatag acat      954
```

<210> 71
<211> 1686
<212> DNA
<213> Canis familiaris

<220>
<221> CDS
<222> (1)..(1683)

<400> 71
```
atg tct atg ctt tca aat gct gag ata aaa gtt aat cct cct cag gat   48
Met Ser Met Leu Ser Asn Ala Glu Ile Lys Val Asn Pro Pro Gln Asp
  1               5                  10                  15
```

```
ttt gag ata gtg gac cct gga tat tta ggt tat ctc tct ttg caa tgg      96
Phe Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr Leu Ser Leu Gln Trp
            20                  25                  30

caa cct cca tta ttt ccg gat aat ttt aag gaa tgc aca ata gaa tat     144
Gln Pro Pro Leu Phe Pro Asp Asn Phe Lys Glu Cys Thr Ile Glu Tyr
            35                  40                  45

gaa tta aaa tac cga aac att gat agt gaa aac tgg aag acc atc att     192
Glu Leu Lys Tyr Arg Asn Ile Asp Ser Glu Asn Trp Lys Thr Ile Ile
        50                  55                  60

acc aag aat cta cat tac aaa gat ggg ttt gat ctt aac aaa ggt att     240
Thr Lys Asn Leu His Tyr Lys Asp Gly Phe Asp Leu Asn Lys Gly Ile
65                  70                  75                  80

gaa gca aag ata aac aca ctt ctg cca gca caa tgc aca aat gga tca     288
Glu Ala Lys Ile Asn Thr Leu Leu Pro Ala Gln Cys Thr Asn Gly Ser
                85                  90                  95

gaa gtt aga agt tca tgg gca gaa act act tat tgg aca tca cca caa     336
Glu Val Arg Ser Ser Trp Ala Glu Thr Thr Tyr Trp Thr Ser Pro Gln
                100                 105                 110

gga aat cgg gaa act aaa att caa gat atg gac tgt gta tat tac aac     384
Gly Asn Arg Glu Thr Lys Ile Gln Asp Met Asp Cys Val Tyr Tyr Asn
            115                 120                 125

tgg caa tat tta gtc tgc tct tgg aaa cct ggc atg ggt gtc cat ttt     432
Trp Gln Tyr Leu Val Cys Ser Trp Lys Pro Gly Met Gly Val His Phe
        130                 135                 140

gat acc aat tac cag ttg ttt tac tgg tat gag ggc ttg gac cat tca     480
Asp Thr Asn Tyr Gln Leu Phe Tyr Trp Tyr Glu Gly Leu Asp His Ser
145                 150                 155                 160

gca gag tgt act gat tac atc aag gtt aat gga aaa aat atg gga tgc     528
Ala Glu Cys Thr Asp Tyr Ile Lys Val Asn Gly Lys Asn Met Gly Cys
                165                 170                 175

agg ttt ccc tat ttg gag tca tca gac tat aaa gat ttc tac atc tgt     576
Arg Phe Pro Tyr Leu Glu Ser Ser Asp Tyr Lys Asp Phe Tyr Ile Cys
                180                 185                 190

gtt aat ggg tca tca gaa tcc cag cct atc aga ccc agc tat ttt att     624
Val Asn Gly Ser Ser Glu Ser Gln Pro Ile Arg Pro Ser Tyr Phe Ile
            195                 200                 205
```

```
ttt cag ctt caa aat ata gtt aaa cct atg cca cca gac tac ctt agt      672
Phe Gln Leu Gln Asn Ile Val Lys Pro Met Pro Pro Asp Tyr Leu Ser
    210                 215                 220


ctt act gtg aag aat tca gag gaa att aac ctg aaa tgg aac atg cct      720
Leu Thr Val Lys Asn Ser Glu Glu Ile Asn Leu Lys Trp Asn Met Pro
225                 230                 235                 240


aaa gga ccc att cca gcc aaa tgt ttc att tat gaa att gaa ttc aca      768
Lys Gly Pro Ile Pro Ala Lys Cys Phe Ile Tyr Glu Ile Glu Phe Thr
                245                 250                 255


gag gat ggt act act tgg gtg act acc aca gtt gag aat gag ata caa      816
Glu Asp Gly Thr Thr Trp Val Thr Thr Thr Val Glu Asn Glu Ile Gln
                260                 265                 270


atc aca aga aca tca aat gaa agc caa aaa tta tgc ttt ttg gta aga      864
Ile Thr Arg Thr Ser Asn Glu Ser Gln Lys Leu Cys Phe Leu Val Arg
            275                 280                 285


agt aaa gtg aat att tat tgc tca gat gat gga atc tgg agt gag tgg      912
Ser Lys Val Asn Ile Tyr Cys Ser Asp Asp Gly Ile Trp Ser Glu Trp
    290                 295                 300


agt gat gaa caa tgc tgg aaa ggt gat atc tgg aag gaa acc gga tcc      960
Ser Asp Glu Gln Cys Trp Lys Gly Asp Ile Trp Lys Glu Thr Gly Ser
305                 310                 315                 320


aac act aaa gta gac aag cca gtg ttc aat gaa tgc aga tgc act gat     1008
Asn Thr Lys Val Asp Lys Pro Val Phe Asn Glu Cys Arg Cys Thr Asp
                325                 330                 335


aca ccc cca tgc cca gtc cct gaa cct ctg gga ggg cct tcg gtc ctc     1056
Thr Pro Pro Cys Pro Val Pro Glu Pro Leu Gly Gly Pro Ser Val Leu
                340                 345                 350


atc ttt ccc ccg aaa ccc aag gac atc ctc agg att acc cga aca ccc     1104
Ile Phe Pro Pro Lys Pro Lys Asp Ile Leu Arg Ile Thr Arg Thr Pro
                355                 360                 365


gag gtc acc tgt gtg gtg tta gat ctg ggc cgt gag gac cct gag gtg     1152
Glu Val Thr Cys Val Val Leu Asp Leu Gly Arg Glu Asp Pro Glu Val
    370                 375                 380


cag atc agc tgg ttc gtg gat ggt aag gag gtg cac aca gcc aag acc     1200
Gln Ile Ser Trp Phe Val Asp Gly Lys Glu Val His Thr Ala Lys Thr
385                 390                 395                 400
```

```
cag tct cgt gag cag cag ttc aac ggc acc tac cgt gtg gtc agc gtc      1248
Gln Ser Arg Glu Gln Gln Phe Asn Gly Thr Tyr Arg Val Val Ser Val
                405                 410                 415

ctc ccc att gag cac cag gac tgg ctc aca ggg aag gag ttc aag tgc      1296
Leu Pro Ile Glu His Gln Asp Trp Leu Thr Gly Lys Glu Phe Lys Cys
                420                 425                 430

aga gtc aac cac ata gac ctc ccg tct ccc atc gag agg acc atc tct      1344
Arg Val Asn His Ile Asp Leu Pro Ser Pro Ile Glu Arg Thr Ile Ser
                435                 440                 445

aag gcc aga ggg agg gcc cat aag ccc agt gtg tat gtc ctg ccg cca      1392
Lys Ala Arg Gly Arg Ala His Lys Pro Ser Val Tyr Val Leu Pro Pro
            450                 455                 460

tcc cca aag gag ttg tca tcc agt gac aca gtc agc atc acc tgc ctg      1440
Ser Pro Lys Glu Leu Ser Ser Ser Asp Thr Val Ser Ile Thr Cys Leu
465                 470                 475                 480

ata aaa gac ttc tac cca cct gac att gat gtg gag tgg cag agc aat      1488
Ile Lys Asp Phe Tyr Pro Pro Asp Ile Asp Val Glu Trp Gln Ser Asn
                485                 490                 495

gga cag cag gag ccc gag agg aag cac cgc atg acc ccg ccc cag ctg      1536
Gly Gln Gln Glu Pro Glu Arg Lys His Arg Met Thr Pro Pro Gln Leu
                500                 505                 510

gac gag gac ggg tcc tac ttc ctg tac agc aag ctc tct gtg gac aag      1584
Asp Glu Asp Gly Ser Tyr Phe Leu Tyr Ser Lys Leu Ser Val Asp Lys
                515                 520                 525

agc cgc tgg cag cag gga gac ccc ttc aca tgt gcg gtg atg cat gaa      1632
Ser Arg Trp Gln Gln Gly Asp Pro Phe Thr Cys Ala Val Met His Glu
            530                 535                 540

act cta cag aac cac tac aca gat cta tcc ctc tcc cat tct ccg ggt      1680
Thr Leu Gln Asn His Tyr Thr Asp Leu Ser Leu Ser His Ser Pro Gly
545                 550                 555                 560

aaa tga                                                               1686
Lys
```

<210> 72
<211> 561
<212> PRT
<213> Canis familiaris

78

<400> 72

Met Ser Met Leu Ser Asn Ala Glu Ile Lys Val Asn Pro Pro Gln Asp
1   5   10   15

Phe Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr Leu Ser Leu Gln Trp
            20   25   30

Gln Pro Pro Leu Phe Pro Asp Asn Phe Lys Glu Cys Thr Ile Glu Tyr
        35   40   45

Glu Leu Lys Tyr Arg Asn Ile Asp Ser Glu Asn Trp Lys Thr Ile Ile
    50   55   60

Thr Lys Asn Leu His Tyr Lys Asp Gly Phe Asp Leu Asn Lys Gly Ile
65   70   75   80

Glu Ala Lys Ile Asn Thr Leu Leu Pro Ala Gln Cys Thr Asn Gly Ser
            85   90   95

Glu Val Arg Ser Ser Trp Ala Glu Thr Thr Tyr Trp Thr Ser Pro Gln
        100   105   110

Gly Asn Arg Glu Thr Lys Ile Gln Asp Met Asp Cys Val Tyr Tyr Asn
        115   120   125

Trp Gln Tyr Leu Val Cys Ser Trp Lys Pro Gly Met Gly Val His Phe
    130   135   140

Asp Thr Asn Tyr Gln Leu Phe Tyr Trp Tyr Glu Gly Leu Asp His Ser
145   150   155   160

Ala Glu Cys Thr Asp Tyr Ile Lys Val Asn Gly Lys Asn Met Gly Cys
            165   170   175

Arg Phe Pro Tyr Leu Glu Ser Ser Asp Tyr Lys Asp Phe Tyr Ile Cys
        180   185   190

Val Asn Gly Ser Ser Glu Ser Gln Pro Ile Arg Pro Ser Tyr Phe Ile
        195   200   205

Phe Gln Leu Gln Asn Ile Val Lys Pro Met Pro Pro Asp Tyr Leu Ser
    210   215   220

Leu Thr Val Lys Asn Ser Glu Glu Ile Asn Leu Lys Trp Asn Met Pro
225   230   235   240

Lys Gly Pro Ile Pro Ala Lys Cys Phe Ile Tyr Glu Ile Glu Phe Thr

79

Glu Asp Gly Thr Thr Trp Val Thr Thr Thr Val Glu Asn Glu Ile Gln
            260   265   270

Ile Thr Arg Thr Ser Asn Glu Ser Gln Lys Leu Cys Phe Leu Val Arg
            275   280   285

Ser Lys Val Asn Ile Tyr Cys Ser Asp Asp Gly Ile Trp Ser Glu Trp
        290   295   300

Ser Asp Glu Gln Cys Trp Lys Gly Asp Ile Trp Lys Glu Thr Gly Ser
305   310   315   320

Asn Thr Lys Val Asp Lys Pro Val Phe Asn Glu Cys Arg Cys Thr Asp
                325   330   335

Thr Pro Pro Cys Pro Val Pro Glu Pro Leu Gly Gly Pro Ser Val Leu
            340   345   350

Ile Phe Pro Pro Lys Pro Lys Asp Ile Leu Arg Ile Thr Arg Thr Pro
            355   360   365

Glu Val Thr Cys Val Val Leu Asp Leu Gly Arg Glu Asp Pro Glu Val
        370   375   380

Gln Ile Ser Trp Phe Val Asp Gly Lys Glu Val His Thr Ala Lys Thr
385   390   395   400

Gln Ser Arg Glu Gln Gln Phe Asn Gly Thr Tyr Arg Val Val Ser Val
            405   410   415

Leu Pro Ile Glu His Gln Asp Trp Leu Thr Gly Lys Glu Phe Lys Cys
            420   425   430

Arg Val Asn His Ile Asp Leu Pro Ser Pro Ile Glu Arg Thr Ile Ser
            435   440   445

Lys Ala Arg Gly Arg Ala His Lys Pro Ser Val Tyr Val Leu Pro Pro
        450   455   460

Ser Pro Lys Glu Leu Ser Ser Ser Asp Thr Val Ser Ile Thr Cys Leu
465   470   475   480

Ile Lys Asp Phe Tyr Pro Pro Asp Ile Asp Val Glu Trp Gln Ser Asn
            485   490   495

Gly Gln Gln Glu Pro Glu Arg Lys His Arg Met Thr Pro Pro Gln Leu

80

Asp Glu Asp Gly Ser Tyr Phe Leu Tyr Ser Lys Leu Ser Val Asp Lys
        515   520   525

Ser Arg Trp Gln Gln Gly Asp Pro Phe Thr Cys Ala Val Met His Glu
    530   535   540

Thr Leu Gln Asn His Tyr Thr Asp Leu Ser Leu Ser His Ser Pro Gly
545   550   555   560

Lys

<210> 73
<211> 1686
<212> DNA
<213> Canis familiaris

<400> 73
tcatttaccc ggagaatggg agagggatag atctgtgtag tggttctgta gagtttcatg 60
catcaccgca catgtgaagg ggtctccctg ctgccagcgg ctcttgtcca cagagagctt 120
gctgtacagg aagtaggacc cgtcctcgtc cagctggggc ggggtcatgc ggtgcttcct 180
ctcgggctcc tgctgtccat tgctctgcca ctccacatca atgtcaggtg ggtagaagtc 240
ttttatcagg caggtgatgc tgactgtgtc actggatgac aactcctttg gggatggcgg 300
caggacatac acactgggct tatgggccct ccctctggcc ttagagatgg tcctctcgat 360
gggagacggg aggtctatgt ggttgactct gcacttgaac tccttccctg tgagccagtc 420
ctggtgctca atggggagga cgctgaccac acggtaggtg ccgttgaact gctgctcacg 480
agactgggtc ttggctgtgt gcacctcctt accatccacg aaccagctga tctgcacctc 540
agggtcctca cggcccagat ctaacaccac acaggtgacc tcgggtgttc gggtaatcct 600
gaggatgtcc ttgggtttcg ggggaaagat gaggaccgaa ggccctccca gaggttcagg 660
gactgggcat gggggtgtat cagtgcatct gcattcattg aacactggct tgtctacttt 720
agtgttggat ccggtttcct tccagatatc acctttccag cattgttcat cactccactc 780
actccagatt ccatcatctg agcaataaat attcacttta cttcttacca aaaagcataa 840
tttttggctt tcatttgatg ttcttgtgat ttgtatctca ttctcaactg tggtagtcac 900
ccaagtagta ccatcctctg tgaattcaat ttcataaatg aaacatttgg ctggaatggg 960
tcctttaggc atgttccatt tcaggttaat ttcctctgaa ttcttcacag taagactaag 1020
gtagtctggt ggcataggtt taactatatt ttgaagctga aaaataaaat agctgggtct 1080
gataggctgg gattctgatg acccattaac acagatgtag aaatctttat agtctgatga 1140
ctccaaatag ggaaacctgc atcccatatt ttttccatta accttgatgt aatcagtaca 1200
ctctgctgaa tggtccaagc cctcatacca gtaaacaac tggtaattgg tatcaaaatg 1260
gacacccatg ccaggtttcc aagagcagac taaatattgc cagttgtaat atacacagtc 1320
catatcttga attttagttt cccgatttcc ttgtggtgat gtccaataag tagtttctgc 1380
ccatgaactt ctaacttctg atccatttgt gcattgtgct ggcagaagtg tgtttatctt 1440
tgcttcaata cctttgttaa gatcaaaccc atctttgtaa tgtagattct tggtaatgat 1500
ggtcttccag ttttcactat caatgtttcg gtattttaat tcatattcta ttgtgcattc 1560

cttaaaatta tccggaaata atggaggttg ccattgcaaa gagagataac ctaaatatcc 1620

agggtccact atctcaaaat cctgaggagg attaactttt atctcagcat ttgaaagcat 1680

agacat   1686

<210> 74

<211> 1698

<212> DNA

<213> Canis familiaris

<220>

<221> CDS

<222> (1)..(1695)

<400> 74

atg tct atg ctt tca aat gct gag ata aaa gtt aat cct cct cag gat   48
Met Ser Met Leu Ser Asn Ala Glu Ile Lys Val Asn Pro Pro Gln Asp
  1   5   10   15

ttt gag ata gtg gac cct gga tat tta ggt tat ctc tct ttg caa tgg   96
Phe Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr Leu Ser Leu Gln Trp
                 20   25   30

caa cct cca tta ttt ccg gat aat ttt aag gaa tgc aca ata gaa tat   144
Gln Pro Pro Leu Phe Pro Asp Asn Phe Lys Glu Cys Thr Ile Glu Tyr
             35   40   45

gaa tta aaa tac cga aac att gat agt gaa aac tgg aag acc atc att   192
Glu Leu Lys Tyr Arg Asn Ile Asp Ser Glu Asn Trp Lys Thr Ile Ile
     50   55   60

acc aag aat cta cat tac aaa gat ggg ttt gat ctt aac aaa ggt att   240
Thr Lys Asn Leu His Tyr Lys Asp Gly Phe Asp Leu Asn Lys Gly Ile
 65   70   75   80

gaa gca aag ata aac aca ctt ctg cca gca caa tgc aca aat gga tca   288
Glu Ala Lys Ile Asn Thr Leu Leu Pro Ala Gln Cys Thr Asn Gly Ser
                 85   90   95

gaa gtt aga agt tca tgg gca gaa act act tat tgg aca tca cca caa   336
Glu Val Arg Ser Ser Trp Ala Glu Thr Thr Tyr Trp Thr Ser Pro Gln
                100   105   110

gga aat cgg gaa act aaa att caa gat atg gac tgt gta tat tac aac   384
Gly Asn Arg Glu Thr Lys Ile Gln Asp Met Asp Cys Val Tyr Tyr Asn
            115   120   125

tgg caa tat tta gtc tgc tct tgg aaa cct ggc atg ggt gtc cat ttt   432

82

Trp Gln Tyr Leu Val Cys Ser Trp Lys Pro Gly Met Gly Val His Phe
    130   135   140

gat acc aat tac cag ttg ttt tac tgg tat gag ggc ttg gac cat tca   480
Asp Thr Asn Tyr Gln Leu Phe Tyr Trp Tyr Glu Gly Leu Asp His Ser
145   150   155   160

gca gag tgt act gat tac atc aag gtt aat gga aaa aat atg gga tgc   528
Ala Glu Cys Thr Asp Tyr Ile Lys Val Asn Gly Lys Asn Met Gly Cys
                165   170   175

agg ttt ccc tat ttg gag tca tca gac tat aaa gat ttc tac atc tgt   576
Arg Phe Pro Tyr Leu Glu Ser Ser Asp Tyr Lys Asp Phe Tyr Ile Cys
                180   185   190

gtt aat ggg tca tca gaa tcc cag cct atc aga ccc agc tat ttt att   624
Val Asn Gly Ser Ser Glu Ser Gln Pro Ile Arg Pro Ser Tyr Phe Ile
                195   200   205

ttt cag ctt caa aat ata gtt aaa cct atg cca cca gac tac ctt agt   672
Phe Gln Leu Gln Asn Ile Val Lys Pro Met Pro Pro Asp Tyr Leu Ser
    210   215   220

ctt act gtg aag aat tca gag gaa att aac ctg aaa tgg aac atg cct   720
Leu Thr Val Lys Asn Ser Glu Glu Ile Asn Leu Lys Trp Asn Met Pro
225   230   235   240

aaa gga ccc att cca gcc aaa tgt ttc att tat gaa att gaa ttc aca   768
Lys Gly Pro Ile Pro Ala Lys Cys Phe Ile Tyr Glu Ile Glu Phe Thr
                245   250   255

gag gat ggt act act tgg gtg act acc aca gtt gag aat gag ata caa   816
Glu Asp Gly Thr Thr Trp Val Thr Thr Thr Val Glu Asn Glu Ile Gln
                260   265   270

atc aca aga aca tca aat gaa agc caa aaa tta tgc ttt ttg gta aga   864
Ile Thr Arg Thr Ser Asn Glu Ser Gln Lys Leu Cys Phe Leu Val Arg
                275   280   285

agt aaa gtg aat att tat tgc tca gat gat gga atc tgg agt gag tgg   912
Ser Lys Val Asn Ile Tyr Cys Ser Asp Asp Gly Ile Trp Ser Glu Trp
    290   295   300

agt gat gaa caa tgc tgg aaa ggt gat atc tgg aag gaa acc gga tcc   960
Ser Asp Glu Gln Cys Trp Lys Gly Asp Ile Trp Lys Glu Thr Gly Ser
305   310   315   320

aac act aaa gta gac aag cca gtg ccc aaa aga gaa aat gga aga gtt   1008

83

Asn Thr Lys Val Asp Lys Pro Val Pro Lys Arg Glu Asn Gly Arg Val
                325   330   335

cct cgc cca cct gat tgt ccc aaa tgc cca gcc cct gaa atg ctg gga   1056
Pro Arg Pro Pro Asp Cys Pro Lys Cys Pro Ala Pro Glu Met Leu Gly
                340   345   350

ggg cct tcg gtc ttc atc ttt ccc ccg aaa ccc aag gac acc ctc ttg   1104
Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Thr Leu Leu
                355   360   365

att gcc cga aca cct gag gtc aca tgt gtg gtg gtg gat ctg gac cca   1152
Ile Ala Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Leu Asp Pro
        370   375   380

gaa gac cct gag gtg cag atc agc tgg ttc gtg gac ggt aag cag atg   1200
Glu Asp Pro Glu Val Gln Ile Ser Trp Phe Val Asp Gly Lys Gln Met
385   390   395   400

caa aca gcc aag act cag cct cgt gag gag cag ttc aat ggc acc tac   1248
Gln Thr Ala Lys Thr Gln Pro Arg Glu Glu Gln Phe Asn Gly Thr Tyr
                405   410   415

cgt gtg gtc agt gtc ctc ccc att ggg cac cag gac tgg ctc aag ggg   1296
Arg Val Val Ser Val Leu Pro Ile Gly His Gln Asp Trp Leu Lys Gly
                420   425   430

aag cag ttc acg tgc aaa gtc aac aac aaa gcc ctc cca tcc ccg atc   1344
Lys Gln Phe Thr Cys Lys Val Asn Asn Lys Ala Leu Pro Ser Pro Ile
                435   440   445

gag agg acc atc tcc aag gcc aga ggg caa gcc cat cag ccc agt gtg   1392
Glu Arg Thr Ile Ser Lys Ala Arg Gly Gln Ala His Gln Pro Ser Val
        450   455   460

tat gtc ctg ccg cca tcc cgg gag gag ttg agc aag aac aca gtc agc   1440
Tyr Val Leu Pro Pro Ser Arg Glu Glu Leu Ser Lys Asn Thr Val Ser
465   470   475   480

ttg aca tgc ctg atc aaa gac ttc ttc cca cct gac att gat gtg gag   1488
Leu Thr Cys Leu Ile Lys Asp Phe Phe Pro Pro Asp Ile Asp Val Glu
                485   490   495

tgg cag agc aat gga cag cag gag cct gag agc aag tac cgc acg acc   1536
Trp Gln Ser Asn Gly Gln Gln Glu Pro Glu Ser Lys Tyr Arg Thr Thr
                500   505   510

ccg ccc cag ctg gac gag gac ggg tcc tac ttc ctg tac agc aag ctc   1584

84

```
Pro Pro Gln Leu Asp Glu Asp Gly Ser Tyr Phe Leu Tyr Ser Lys Leu
        515                 520                 525

tct gtg gac aag agc cgc tgg cag cgg gga gac acc ttc ata tgt gcg      1632
Ser Val Asp Lys Ser Arg Trp Gln Arg Gly Asp Thr Phe Ile Cys Ala
        530                 535                 540

gtg atg cat gaa gct cta cac aac cac tac aca cag gaa tcc ctc tcc      1680
Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Glu Ser Leu Ser
545                 550                 555                 560

cat tct ccg ggt aaa tga                                              1698
His Ser Pro Gly Lys
                565
```

<210> 75
<211> 565
<212> PRT
<213> Canis familiaris

<400> 75

```
Met Ser Met Leu Ser Asn Ala Glu Ile Lys Val Asn Pro Pro Gln Asp
 1               5                  10                  15

Phe Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr Leu Ser Leu Gln Trp
            20                  25                  30

Gln Pro Pro Leu Phe Pro Asp Asn Phe Lys Glu Cys Thr Ile Glu Tyr
        35                  40                  45

Glu Leu Lys Tyr Arg Asn Ile Asp Ser Glu Asn Trp Lys Thr Ile Ile
    50                  55                  60

Thr Lys Asn Leu His Tyr Lys Asp Gly Phe Asp Leu Asn Lys Gly Ile
65                  70                  75                  80

Glu Ala Lys Ile Asn Thr Leu Leu Pro Ala Gln Cys Thr Asn Gly Ser
                85                  90                  95

Glu Val Arg Ser Ser Trp Ala Glu Thr Thr Tyr Trp Thr Ser Pro Gln
            100                 105                 110

Gly Asn Arg Glu Thr Lys Ile Gln Asp Met Asp Cys Val Tyr Tyr Asn
            115                 120                 125

Trp Gln Tyr Leu Val Cys Ser Trp Lys Pro Gly Met Gly Val His Phe
        130                 135                 140
```

Asp Thr Asn Tyr Gln Leu Phe Tyr Trp Tyr Glu Gly Leu Asp His Ser
145   150   155   160

Ala Glu Cys Thr Asp Tyr Ile Lys Val Asn Gly Lys Asn Met Gly Cys
                165   170   175

Arg Phe Pro Tyr Leu Glu Ser Ser Asp Tyr Lys Asp Phe Tyr Ile Cys
                180   185   190

Val Asn Gly Ser Ser Glu Ser Gln Pro Ile Arg Pro Ser Tyr Phe Ile
                195   200   205

Phe Gln Leu Gln Asn Ile Val Lys Pro Met Pro Pro Asp Tyr Leu Ser
        210   215   220

Leu Thr Val Lys Asn Ser Glu Glu Ile Asn Leu Lys Trp Asn Met Pro
225   230   235   240

Lys Gly Pro Ile Pro Ala Lys Cys Phe Ile Tyr Glu Ile Glu Phe Thr
                245   250   255

Glu Asp Gly Thr Thr Trp Val Thr Thr Thr Val Glu Asn Glu Ile Gln
                260   265   270

Ile Thr Arg Thr Ser Asn Glu Ser Gln Lys Leu Cys Phe Leu Val Arg
                275   280   285

Ser Lys Val Asn Ile Tyr Cys Ser Asp Asp Gly Ile Trp Ser Glu Trp
        290   295   300

Ser Asp Glu Gln Cys Trp Lys Gly Asp Ile Trp Lys Glu Thr Gly Ser
305   310   315   320

Asn Thr Lys Val Asp Lys Pro Val Pro Lys Arg Glu Asn Gly Arg Val
                325   330   335

Pro Arg Pro Pro Asp Cys Pro Lys Cys Pro Ala Pro Glu Met Leu Gly
                340   345   350

Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Thr Leu Leu
        355   360   365

Ile Ala Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Leu Asp Pro
        370   375   380

Glu Asp Pro Glu Val Gln Ile Ser Trp Phe Val Asp Gly Lys Gln Met
385   390   395   400

86

Gln Thr Ala Lys Thr Gln Pro Arg Glu Glu Gln Phe Asn Gly Thr Tyr
                405   410   415

Arg Val Val Ser Val Leu Pro Ile Gly His Gln Asp Trp Leu Lys Gly
                420   425   430

Lys Gln Phe Thr Cys Lys Val Asn Asn Lys Ala Leu Pro Ser Pro Ile
                435   440   445

Glu Arg Thr Ile Ser Lys Ala Arg Gly Gln Ala His Gln Pro Ser Val
            450   455   460

Tyr Val Leu Pro Pro Ser Arg Glu Glu Leu Ser Lys Asn Thr Val Ser
465   470   475   480

Leu Thr Cys Leu Ile Lys Asp Phe Phe Pro Pro Asp Ile Asp Val Glu
                485   490   495

Trp Gln Ser Asn Gly Gln Gln Glu Pro Glu Ser Lys Tyr Arg Thr Thr
                500   505   510

Pro Pro Gln Leu Asp Glu Asp Gly Ser Tyr Phe Leu Tyr Ser Lys Leu
                515   520   525

Ser Val Asp Lys Ser Arg Trp Gln Arg Gly Asp Thr Phe Ile Cys Ala
            530   535   540

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Glu Ser Leu Ser
545   550   555   560

His Ser Pro Gly Lys
                565

<210> 76
<211> 1698
<212> DNA
<213> Canis familiaris

<400> 76
tcatttaccc ggagaatggg agagggattc ctgtgtgtag tggttgtgta gagcttcatg 60
catcaccgca catatgaagg tgtctccccg ctgccagcgg ctcttgtcca cagagagctt 120
gctgtacagg aagtaggacc cgtcctcgtc cagctggggc ggggtcgtgc ggtacttgct 180
ctcaggctcc tgctgtccat tgctctgcca ctccacatca atgtcaggtg ggaagaagtc 240
tttgatcagg catgtcaagc tgactgtgtt cttgctcaac tcctcccggg atggcggcag 300
gacatacaca ctgggctgat gggcttgccc tctggccttg agatggtccc tctcgatcgg 360

87

```
ggatgggagg gctttgttgt tgactttgca cgtgaactgc ttccccttga gccagtcctg 420
gtgcccaatg gggaggacac tgaccacacg gtaggtgcca ttgaactgct cctcacgagg 480
ctgagtcttg gctgtttgca tctgcttacc gtccacgaac cagctgatct gcacctcagg 540
gtcttctggg tccagatcca ccaccacaca tgtgacctca ggtgttcggg caatcaagag 600
ggtgtccttg ggtttcgggg gaaagatgaa gaccgaaggc cctcccagca tttcaggggc 660
tgggcatttg ggacaatcag gtgggcgagg aactcttcca ttttctcttt tgggcactgg 720
cttgtctact ttagtgttgg atccggtttc cttccagata tcacctttcc agcattgttc 780
atcactccac tcactccaga ttccatcatc tgagcaataa atattcactt tacttcttac 840
caaaaagcat aattttggc tttcatttga tgttcttgtg atttgtatct cattctcaac 900
tgtggtagtc acccaagtag taccatcctc tgtgaattca atttcataaa tgaaacattt 960
ggctggaatg ggtcctttag gcatgttcca tttcaggtta atttcctctg aattcttcac 1020
agtaagacta aggtagtctg gtggcatagg tttaactata ttttgaagct gaaaaataaa 1080
atagctgggt ctgataggct gggattctga tgacccatta acacagatgt agaaatcttt 1140
atagtctgat gactccaaat agggaaacct gcatcccata ttttttccat taaccttgat 1200
gtaatcagta cactctgctg aatggtccaa gccctcatac cagtaaaaca actggtaatt 1260
ggtatcaaaa tggacaccca tgccaggttt ccaagagcag actaaatatt gccagttgta 1320
atatacacag tccatatctt gaattttagt ttcccgattt ccttgtggtg atgtccaata 1380
agtagtttct gcccatgaac ttctaacttc tgatccattt gtgcattgtg ctggcagaag 1440
tgtgtttatc tttgcttcaa tacctttgtt aagatcaaac ccatctttgt aatgtagatt 1500
cttggtaatg atggtcttcc agttttcact atcaatgttt cggtatttta attcatattc 1560
tattgtgcat tccttaaaat tatccggaaa taatggaggt tgccattgca aagagagata 1620
acctaaatat ccagggtcca ctatctcaaa atcctgagga ggattaactt ttatctcagc 1680
atttgaaagc atagacat                                                1698
```

```
atg tct atg ctt tca aat gct gag ata aaa gtt aat cct cct cag gat      48
Met Ser Met Leu Ser Asn Ala Glu Ile Lys Val Asn Pro Pro Gln Asp
  1               5                  10                  15

ttt gag ata gtg gac cct gga tat tta ggt tat ctc tct ttg caa tgg      96
Phe Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr Leu Ser Leu Gln Trp
             20                  25                  30

caa cct cca tta ttt ccg gat aat ttt aag gaa tgc aca ata gaa tat     144
Gln Pro Pro Leu Phe Pro Asp Asn Phe Lys Glu Cys Thr Ile Glu Tyr
         35                  40                  45

gaa tta aaa tac cga aac att gat agt gaa aac tgg aag acc atc att     192
```

```
Glu Leu Lys Tyr Arg Asn Ile Asp Ser Glu Asn Trp Lys Thr Ile Ile
        50                  55                  60


acc aag aat cta cat tac aaa gat ggg ttt gat ctt aac aaa ggt att      240
Thr Lys Asn Leu His Tyr Lys Asp Gly Phe Asp Leu Asn Lys Gly Ile
 65              70                  75                  80


gaa gca aag ata aac aca ctt ctg cca gca caa tgc aca aat gga tca      288
Glu Ala Lys Ile Asn Thr Leu Leu Pro Ala Gln Cys Thr Asn Gly Ser
                85                  90                  95


gaa gtt aga agt tca tgg gca gaa act act tat tgg aca tca cca caa      336
Glu Val Arg Ser Ser Trp Ala Glu Thr Thr Tyr Trp Thr Ser Pro Gln
            100                 105                 110


gga aat cgg gaa act aaa att caa gat atg gac tgt gta tat tac aac      384
Gly Asn Arg Glu Thr Lys Ile Gln Asp Met Asp Cys Val Tyr Tyr Asn
            115                 120                 125


tgg caa tat tta gtc tgc tct tgg aaa cct ggc atg ggt gtc cat ttt      432
Trp Gln Tyr Leu Val Cys Ser Trp Lys Pro Gly Met Gly Val His Phe
        130                 135                 140


gat acc aat tac cag ttg ttt tac tgg tat gag ggc ttg gac cat tca      480
Asp Thr Asn Tyr Gln Leu Phe Tyr Trp Tyr Glu Gly Leu Asp His Ser
145                 150                 155                 160


gca gag tgt act gat tac atc aag gtt aat gga aaa aat atg gga tgc      528
Ala Glu Cys Thr Asp Tyr Ile Lys Val Asn Gly Lys Asn Met Gly Cys
                165                 170                 175


agg ttt ccc tat ttg gag tca tca gac tat aaa gat ttc tac atc tgt      576
Arg Phe Pro Tyr Leu Glu Ser Ser Asp Tyr Lys Asp Phe Tyr Ile Cys
            180                 185                 190


gtt aat ggg tca tca gaa tcc cag cct atc aga ccc agc tat ttt att      624
Val Asn Gly Ser Ser Glu Ser Gln Pro Ile Arg Pro Ser Tyr Phe Ile
            195                 200                 205


ttt cag ctt caa aat ata gtt aaa cct atg cca cca gac tac ctt agt      672
Phe Gln Leu Gln Asn Ile Val Lys Pro Met Pro Pro Asp Tyr Leu Ser
        210                 215                 220


ctt act gtg aag aat tca gag gaa att aac ctg aaa tgg aac atg cct      720
Leu Thr Val Lys Asn Ser Glu Glu Ile Asn Leu Lys Trp Asn Met Pro
225                 230                 235                 240


aaa gga ccc att cca gcc aaa tgt ttc att tat gaa att gaa ttc aca      768
```

89

```
Lys Gly Pro Ile Pro Ala Lys Cys Phe Ile Tyr Glu Ile Glu Phe Thr
                245                 250                 255


gag gat ggt act act tgg gtg act acc aca gtt gag aat gag ata caa    816
Glu Asp Gly Thr Thr Trp Val Thr Thr Thr Val Glu Asn Glu Ile Gln
            260                 265                 270


atc aca aga aca tca aat gaa agc caa aaa tta tgc ttt ttg gta aga    864
Ile Thr Arg Thr Ser Asn Glu Ser Gln Lys Leu Cys Phe Leu Val Arg
        275                 280                 285


agt aaa gtg aat att tat tgc tca gat gat gga atc tgg agt gag tgg    912
Ser Lys Val Asn Ile Tyr Cys Ser Asp Asp Gly Ile Trp Ser Glu Trp
    290                 295                 300


agt gat gaa caa tgc tgg aaa ggt gat atc tgg aag gaa acc gga tcc    960
Ser Asp Glu Gln Cys Trp Lys Gly Asp Ile Trp Lys Glu Thr Gly Ser
305                 310                 315                 320


aac act aaa gta gac aag cca gtg gcc aaa gaa tgc gag tgc aag tgt   1008
Asn Thr Lys Val Asp Lys Pro Val Ala Lys Glu Cys Glu Cys Lys Cys
                325                 330                 335


aac tgt aac aac tgc cca tgc cca ggt tgt ggc ctg ctg gga ggg cct   1056
Asn Cys Asn Asn Cys Pro Cys Pro Gly Cys Gly Leu Leu Gly Gly Pro
            340                 345                 350


tcg gtc ttc atc ttt ccc cca aaa ccc aag gac atc ctc gtg act gcc   1104
Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Ile Leu Val Thr Ala
        355                 360                 365


cgg aca ccc aca gtc act tgt gtg gtg gtg gat ctg gac cca gaa aac   1152
Arg Thr Pro Thr Val Thr Cys Val Val Val Asp Leu Asp Pro Glu Asn
    370                 375                 380


cct gag gtg cag atc agc tgg ttc gtg gat agt aag cag gtg caa aca   1200
Pro Glu Val Gln Ile Ser Trp Phe Val Asp Ser Lys Gln Val Gln Thr
385                 390                 395                 400


gcc aac acg cag cct cgt gag gag cag tcc aat ggc acc tac cgt gtg   1248
Ala Asn Thr Gln Pro Arg Glu Glu Gln Ser Asn Gly Thr Tyr Arg Val
                405                 410                 415


gtc agt gtc ctc ccc att ggg cac cag gac tgg ctt tca ggg aag cag   1296
Val Ser Val Leu Pro Ile Gly His Gln Asp Trp Leu Ser Gly Lys Gln
            420                 425                 430


ttc aag tgc aaa gtc aac aac aaa gcc ctc cca tcc ccc att gag gag   1344
```

90

```
Phe Lys Cys Lys Val Asn Asn Lys Ala Leu Pro Ser Pro Ile Glu Glu
        435                 440                 445

atc atc tcc aag acc cca ggg cag gcc cat cag cct aat gtg tat gtc      1392
Ile Ile Ser Lys Thr Pro Gly Gln Ala His Gln Pro Asn Val Tyr Val
        450                 455                 460

ctg ccg cca tcg cgg gat gag atg agc aag aat acg gtc acc ctg acc      1440
Leu Pro Pro Ser Arg Asp Glu Met Ser Lys Asn Thr Val Thr Leu Thr
465                 470                 475                 480

tgt ctg gtc aaa gac ttc ttc cca cct gag att gat gtg gag tgg cag      1488
Cys Leu Val Lys Asp Phe Phe Pro Pro Glu Ile Asp Val Glu Trp Gln
                485                 490                 495

agc aat gga cag cag gag cct gag agc aag tac cgc atg acc ccg ccc      1536
Ser Asn Gly Gln Gln Glu Pro Glu Ser Lys Tyr Arg Met Thr Pro Pro
                500                 505                 510

cag ctg gat gaa gat ggg tcc tac ttc cta tac agc aag ctc tcc gtg      1584
Gln Leu Asp Glu Asp Gly Ser Tyr Phe Leu Tyr Ser Lys Leu Ser Val
            515                 520                 525

gac aag agc cgc tgg cag cgg gga gac acc ttc ata tgt gcg gtg atg      1632
Asp Lys Ser Arg Trp Gln Arg Gly Asp Thr Phe Ile Cys Ala Val Met
        530                 535                 540

cat gaa gct cta cac aac cac tac aca cag ata tcc ctc tcc cat tct      1680
His Glu Ala Leu His Asn His Tyr Thr Gln Ile Ser Leu Ser His Ser
545                 550                 555                 560

ccg ggt aaa tga                                                       1692
Pro Gly Lys


<210> 78
<211> 563
<212> PRT
<213> Canis familiaris

<400> 78
Met Ser Met Leu Ser Asn Ala Glu Ile Lys Val Asn Pro Pro Gln Asp
  1               5                  10                  15

Phe Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr Leu Ser Leu Gln Trp
            20                  25                  30

Gln Pro Pro Leu Phe Pro Asp Asn Phe Lys Glu Cys Thr Ile Glu Tyr
```

91

Glu Leu Lys Tyr Arg Asn Ile Asp Ser Glu Asn Trp Lys Thr Ile Ile
    50   55   60

Thr Lys Asn Leu His Tyr Lys Asp Gly Phe Asp Leu Asn Lys Gly Ile
65   70   75   80

Glu Ala Lys Ile Asn Thr Leu Leu Pro Ala Gln Cys Thr Asn Gly Ser
                85   90   95

Glu Val Arg Ser Ser Trp Ala Glu Thr Thr Tyr Trp Thr Ser Pro Gln
            100   105   110

Gly Asn Arg Glu Thr Lys Ile Gln Asp Met Asp Cys Val Tyr Tyr Asn
            115   120   125

Trp Gln Tyr Leu Val Cys Ser Trp Lys Pro Gly Met Gly Val His Phe
        130   135   140

Asp Thr Asn Tyr Gln Leu Phe Tyr Trp Tyr Glu Gly Leu Asp His Ser
145   150   155   160

Ala Glu Cys Thr Asp Tyr Ile Lys Val Asn Gly Lys Asn Met Gly Cys
                165   170   175

Arg Phe Pro Tyr Leu Glu Ser Ser Asp Tyr Lys Asp Phe Tyr Ile Cys
            180   185   190

Val Asn Gly Ser Ser Glu Ser Gln Pro Ile Arg Pro Ser Tyr Phe Ile
            195   200   205

Phe Gln Leu Gln Asn Ile Val Lys Pro Met Pro Pro Asp Tyr Leu Ser
    210   215   220

Leu Thr Val Lys Asn Ser Glu Glu Ile Asn Leu Lys Trp Asn Met Pro
225   230   235   240

Lys Gly Pro Ile Pro Ala Lys Cys Phe Ile Tyr Glu Ile Glu Phe Thr
                245   250   255

Glu Asp Gly Thr Thr Trp Val Thr Thr Val Glu Asn Glu Ile Gln
            260   265   270

Ile Thr Arg Thr Ser Asn Glu Ser Gln Lys Leu Cys Phe Leu Val Arg
            275   280   285

Ser Lys Val Asn Ile Tyr Cys Ser Asp Asp Gly Ile Trp Ser Glu Trp

Ser Asp Glu Gln Cys Trp Lys Gly Asp Ile Trp Lys Glu Thr Gly Ser
305   310   315   320

Asn Thr Lys Val Asp Lys Pro Val Ala Lys Glu Cys Glu Cys Lys Cys
                   325   330   335

Asn Cys Asn Asn Cys Pro Cys Pro Gly Cys Gly Leu Leu Gly Gly Pro
                   340   345   350

Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Ile Leu Val Thr Ala
                   355   360   365

Arg Thr Pro Thr Val Thr Cys Val Val Val Asp Leu Asp Pro Glu Asn
370   375   380

Pro Glu Val Gln Ile Ser Trp Phe Val Asp Ser Lys Gln Val Gln Thr
385   390   395   400

Ala Asn Thr Gln Pro Arg Glu Glu Gln Ser Asn Gly Thr Tyr Arg Val
                   405   410   415

Val Ser Val Leu Pro Ile Gly His Gln Asp Trp Leu Ser Gly Lys Gln
                   420   425   430

Phe Lys Cys Lys Val Asn Asn Lys Ala Leu Pro Ser Pro Ile Glu Glu
                   435   440   445

Ile Ile Ser Lys Thr Pro Gly Gln Ala His Gln Pro Asn Val Tyr Val
                   450   455   460

Leu Pro Pro Ser Arg Asp Glu Met Ser Lys Asn Thr Val Thr Leu Thr
465   470   475   480

Cys Leu Val Lys Asp Phe Phe Pro Pro Glu Ile Asp Val Glu Trp Gln
                   485   490   495

Ser Asn Gly Gln Gln Glu Pro Glu Ser Lys Tyr Arg Met Thr Pro Pro
                   500   505   510

Gln Leu Asp Glu Asp Gly Ser Tyr Phe Leu Tyr Ser Lys Leu Ser Val
                   515   520   525

Asp Lys Ser Arg Trp Gln Arg Gly Asp Thr Phe Ile Cys Ala Val Met
                   530   535   540

His Glu Ala Leu His Asn His Tyr Thr Gln Ile Ser Leu Ser His Ser

Pro Gly Lys

<210> 79
<211> 1692
<212> DNA
<213> Canis familiaris

<400> 79
tcatttaccc ggagaatggg agagggatat ctgtgtgtag tggttgtgta gagcttcatg 60
catcaccgca catatgaagg tgtctccccg ctgccagcgg ctcttgtcca cggagagctt 120
gctgtatagg aagtaggacc catcttcatc cagctggggc ggggtcatgc ggtacttgct 180
ctcaggctcc tgctgtccat tgctctgcca ctccacatca atctcaggtg ggaagaagtc 240
tttgaccaga caggtcaggg tgaccgtatt cttgctcatc tcatcccgcg atggcggcag 300
gacatacaca ttaggctgat gggcctgccc tggggtcttg agatgatct cctcaatggg 360
ggatgggagg gctttgttgt tgactttgca cttgaactgc ttccctgaaa gccagtcctg 420
gtgcccaatg gggaggacac tgaccacacg gtaggtgcca ttggactgct cctcacgagg 480
ctgcgtgttg gctgtttgca cctgcttact atccacgaac cagctgatct gcacctcagg 540
gttttctggg tccagatcca ccaccacaca agtgactgtg ggtgtccggg cagtcacgag 600
gatgtccttg ggttttgggg gaaagatgaa gaccgaaggc cctcccagca ggccacaacc 660
tgggcatggg cagttgttac agttacactt gcactcgcat tctttggcca ctggcttgtc 720
tactttagtg ttggatccgg tttccttcca gatatcacct ttccagcatt gttcatcact 780
ccactcactc cagattccat catctgagca ataaatattc actttacttc ttaccaaaaa 840
gcataatttt tggctttcat ttgatgttct tgtgatttgt atctcattct caactgtggt 900
agtcacccaa gtagtaccat cctctgtgaa ttcaatttca taaatgaaac atttggctgg 960
aatgggtcct ttaggcatgt tccatttcag gttaatttcc tctgaattct tcacagtaag 1020
actaaggtag tctggtggca taggtttaac tatattttga agctgaaaaa taaaatagct 1080
gggtctgata ggctgggatt ctgatgaccc attaacacag atgtagaaat ctttatagtc 1140
tgatgactcc aaatagggaa acctgcatcc catattttt ccattaacct tgatgtaatc 1200
agtacactct gctgaatggt ccaagccctc ataccagtaa aacaactggt aattggtatc 1260
aaaatggaca cccatgccag gtttccaaga gcagactaaa tattgccagt tgtaatatac 1320
acagtccata tcttgaattt tagtttcccg atttccttgt ggtgatgtcc aataagtagt 1380
ttctgcccat gaacttctaa cttctgatcc atttgtgcat tgtgctggca gaagtgtgtt 1440
tatctttgct tcaatacctt tgttaagatc aaacccatct ttgtaatgta gattcttggt 1500
aatgatggtc ttccagtttt cactatcaat gtttcggtat tttaattcat attctattgt 1560
gcattcctta aaattatccg gaaataatgg aggttgccat tgcaaagaga gataacctaa 1620
atatccaggg tccactatct caaaatcctg aggaggatta acttttatct cagcatttga 1680
aagcatagac at 1692

<210> 80
<211> 1686
<212> DNA
<213> Canis familiaris

<220>
<221> CDS
<222> (1)..(1683)

<400> 80
atg tct atg ctt tca aat gct gag ata aaa gtt aat cct cct cag gat   48
Met Ser Met Leu Ser Asn Ala Glu Ile Lys Val Asn Pro Pro Gln Asp
1   5   10   15

ttt gag ata gtg gac cct gga tat tta ggt tat ctc tct ttg caa tgg   96
Phe Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr Leu Ser Leu Gln Trp
                20   25   30

caa cct cca tta ttt ccg gat aat ttt aag gaa tgc aca ata gaa tat   144
Gln Pro Pro Leu Phe Pro Asp Asn Phe Lys Glu Cys Thr Ile Glu Tyr
            35   40   45

gaa tta aaa tac cga aac att gat agt gaa aac tgg aag acc atc att   192
Glu Leu Lys Tyr Arg Asn Ile Asp Ser Glu Asn Trp Lys Thr Ile Ile
        50   55   60

acc aag aat cta cat tac aaa gat ggg ttt gat ctt aac aaa ggt att   240
Thr Lys Asn Leu His Tyr Lys Asp Gly Phe Asp Leu Asn Lys Gly Ile
65   70   75   80

gaa gca aag ata aac aca ctt ctg cca gca caa tgc aca aat gga tca   288
Glu Ala Lys Ile Asn Thr Leu Leu Pro Ala Gln Cys Thr Asn Gly Ser
                85   90   95

gaa gtt aga agt tca tgg gca gaa act act tat tgg aca tca cca caa   336
Glu Val Arg Ser Ser Trp Ala Glu Thr Thr Tyr Trp Thr Ser Pro Gln
            100   105   110

gga aat cgg gaa act aaa att caa gat atg gac tgt gta tat tac aac   384
Gly Asn Arg Glu Thr Lys Ile Gln Asp Met Asp Cys Val Tyr Tyr Asn
            115   120   125

tgg caa tat tta gtc tgc tct tgg aaa cct ggc atg ggt gtc cat ttt   432
Trp Gln Tyr Leu Val Cys Ser Trp Lys Pro Gly Met Gly Val His Phe
        130   135   140

gat acc aat tac cag ttg ttt tac tgg tat gag ggc ttg gac cat tca   480
Asp Thr Asn Tyr Gln Leu Phe Tyr Trp Tyr Glu Gly Leu Asp His Ser
145   150   155   160

gca gag tgt act gat tac atc aag gtt aat gga aaa aat atg gga tgc   528
Ala Glu Cys Thr Asp Tyr Ile Lys Val Asn Gly Lys Asn Met Gly Cys

95

```
agg ttt ccc tat ttg gag tca tca gac tat aaa gat ttc tac atc tgt    576
Arg Phe Pro Tyr Leu Glu Ser Ser Asp Tyr Lys Asp Phe Tyr Ile Cys
            180             185             190

gtt aat ggg tca tca gaa tcc cag cct atc aga ccc agc tat ttt att    624
Val Asn Gly Ser Ser Glu Ser Gln Pro Ile Arg Pro Ser Tyr Phe Ile
        195             200             205

ttt cag ctt caa aat ata gtt aaa cct atg cca cca gac tac ctt agt    672
Phe Gln Leu Gln Asn Ile Val Lys Pro Met Pro Pro Asp Tyr Leu Ser
    210             215             220

ctt act gtg aag aat tca gag gaa att aac ctg aaa tgg aac atg cct    720
Leu Thr Val Lys Asn Ser Glu Glu Ile Asn Leu Lys Trp Asn Met Pro
225             230             235             240

aaa gga ccc att cca gcc aaa tgt ttc att tat gaa att gaa ttc aca    768
Lys Gly Pro Ile Pro Ala Lys Cys Phe Ile Tyr Glu Ile Glu Phe Thr
                245             250             255

gag gat ggt act act tgg gtg act acc aca gtt gag aat gag ata caa    816
Glu Asp Gly Thr Thr Trp Val Thr Thr Thr Val Glu Asn Glu Ile Gln
            260             265             270

atc aca aga aca tca aat gaa agc caa aaa tta tgc ttt ttg gta aga    864
Ile Thr Arg Thr Ser Asn Glu Ser Gln Lys Leu Cys Phe Leu Val Arg
            275             280             285

agt aaa gtg aat att tat tgc tca gat gat gga atc tgg agt gag tgg    912
Ser Lys Val Asn Ile Tyr Cys Ser Asp Asp Gly Ile Trp Ser Glu Trp
    290             295             300

agt gat gaa caa tgc tgg aaa ggt gat atc tgg aag gaa acc gga tcc    960
Ser Asp Glu Gln Cys Trp Lys Gly Asp Ile Trp Lys Glu Thr Gly Ser
305             310             315             320

aac act aaa gta gac aag cca gtg ccc aaa gag tcc acc tgc aag tgt   1008
Asn Thr Lys Val Asp Lys Pro Val Pro Lys Glu Ser Thr Cys Lys Cys
                325             330             335

ata tcc cca tgc cca gtc cct gaa tca ctg gga ggg cct tcg gtc ttc   1056
Ile Ser Pro Cys Pro Val Pro Glu Ser Leu Gly Gly Pro Ser Val Phe
                340             345             350

atc ttt ccc ccg aaa ccc aag gac atc ctc agg att acc cga aca ccc   1104
Ile Phe Pro Pro Lys Pro Lys Asp Ile Leu Arg Ile Thr Arg Thr Pro
```

gag atc acc tgt gtg gtg tta gat ctg ggc cgt gag gac cct gag gtg   1152
Glu Ile Thr Cys Val Val Leu Asp Leu Gly Arg Glu Asp Pro Glu Val
      370   375   380

cag atc agc tgg ttc gtg gat ggt aag gag gtg cac aca gcc aag acg   1200
Gln Ile Ser Trp Phe Val Asp Gly Lys Glu Val His Thr Ala Lys Thr
385   390   395   400

cag cct cgt gag cag cag ttc aac agc acc tac cgt gtg gtc agc gtc   1248
Gln Pro Arg Glu Gln Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val
                405   410   415

ctc ccc att gag cac cag gac tgg ctc acc gga aag gag ttc aag tgc   1296
Leu Pro Ile Glu His Gln Asp Trp Leu Thr Gly Lys Glu Phe Lys Cys
                420   425   430

aga gtc aac cac ata ggc ctc ccg tcc ccc atc gag agg act atc tcc   1344
Arg Val Asn His Ile Gly Leu Pro Ser Pro Ile Glu Arg Thr Ile Ser
      435   440   445

aaa gcc aga ggg caa gcc cat cag ccc agt gtg tat gtc ctg cca cca   1392
Lys Ala Arg Gly Gln Ala His Gln Pro Ser Val Tyr Val Leu Pro Pro
      450   455   460

tcc cca aag gag ttg tca tcc agt gac acg gtc acc ctg acc tgc ctg   1440
Ser Pro Lys Glu Leu Ser Ser Ser Asp Thr Val Thr Leu Thr Cys Leu
465   470   475   480

atc aaa gac ttc ttc cca cct gag att gat gtg gag tgg cag agc aat   1488
Ile Lys Asp Phe Phe Pro Pro Glu Ile Asp Val Glu Trp Gln Ser Asn
                485   490   495

gga cag ccg gag ccc gag agc aag tac cac acg act gcg ccc cag ctg   1536
Gly Gln Pro Glu Pro Glu Ser Lys Tyr His Thr Thr Ala Pro Gln Leu
                500   505   510

gac gag gac ggg tcc tac ttc ctg tac agc aag ctc tct gtg gac aag   1584
Asp Glu Asp Gly Ser Tyr Phe Leu Tyr Ser Lys Leu Ser Val Asp Lys
                515   520   525

agc cgc tgg cag cag gga gac acc ttc aca tgt gcg gtg atg cat gaa   1632
Ser Arg Trp Gln Gln Gly Asp Thr Phe Thr Cys Ala Val Met His Glu
      530   535   540

gct cta cag aac cac tac aca gat cta tcc ctc tcc cat tct ccg ggt   1680
Ala Leu Gln Asn His Tyr Thr Asp Leu Ser Leu Ser His Ser Pro Gly

97

aaa tga   1686
Lys

<210> 81
<211> 561
<212> PRT
<213> Canis familiaris

<400> 81
Met Ser Met Leu Ser Asn Ala Glu Ile Lys Val Asn Pro Pro Gln Asp
 1   5   10   15

Phe Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr Leu Ser Leu Gln Trp
             20   25   30

Gln Pro Pro Leu Phe Pro Asp Asn Phe Lys Glu Cys Thr Ile Glu Tyr
         35   40   45

Glu Leu Lys Tyr Arg Asn Ile Asp Ser Glu Asn Trp Lys Thr Ile Ile
     50   55   60

Thr Lys Asn Leu His Tyr Lys Asp Gly Phe Asp Leu Asn Lys Gly Ile
 65   70   75   80

Glu Ala Lys Ile Asn Thr Leu Leu Pro Ala Gln Cys Thr Asn Gly Ser
                 85   90   95

Glu Val Arg Ser Ser Trp Ala Glu Thr Thr Tyr Trp Thr Ser Pro Gln
             100   105   110

Gly Asn Arg Glu Thr Lys Ile Gln Asp Met Asp Cys Val Tyr Tyr Asn
             115   120   125

Trp Gln Tyr Leu Val Cys Ser Trp Lys Pro Gly Met Gly Val His Phe
     130   135   140

Asp Thr Asn Tyr Gln Leu Phe Tyr Trp Tyr Glu Gly Leu Asp His Ser
145   150   155   160

Ala Glu Cys Thr Asp Tyr Ile Lys Val Asn Gly Lys Asn Met Gly Cys
                 165   170   175

Arg Phe Pro Tyr Leu Glu Ser Ser Asp Tyr Lys Asp Phe Tyr Ile Cys
             180   185   190

98

Val Asn Gly Ser Ser Glu Ser Gln Pro Ile Arg Pro Ser Tyr Phe Ile
        195   200   205

Phe Gln Leu Gln Asn Ile Val Lys Pro Met Pro Pro Asp Tyr Leu Ser
        210   215   220

Leu Thr Val Lys Asn Ser Glu Glu Ile Asn Leu Lys Trp Asn Met Pro
225   230   235   240

Lys Gly Pro Ile Pro Ala Lys Cys Phe Ile Tyr Glu Ile Glu Phe Thr
                245   250   255

Glu Asp Gly Thr Thr Trp Val Thr Thr Thr Val Glu Asn Glu Ile Gln
                260   265   270

Ile Thr Arg Thr Ser Asn Glu Ser Gln Lys Leu Cys Phe Leu Val Arg
        275   280   285

Ser Lys Val Asn Ile Tyr Cys Ser Asp Asp Gly Ile Trp Ser Glu Trp
        290   295   300

Ser Asp Glu Gln Cys Trp Lys Gly Asp Ile Trp Lys Glu Thr Gly Ser
305   310   315   320

Asn Thr Lys Val Asp Lys Pro Val Pro Lys Glu Ser Thr Cys Lys Cys
                325   330   335

Ile Ser Pro Cys Pro Val Pro Glu Ser Leu Gly Gly Pro Ser Val Phe
                340   345   350

Ile Phe Pro Pro Lys Pro Lys Asp Ile Leu Arg Ile Thr Arg Thr Pro
                355   360   365

Glu Ile Thr Cys Val Val Leu Asp Leu Gly Arg Glu Asp Pro Glu Val
        370   375   380

Gln Ile Ser Trp Phe Val Asp Gly Lys Glu Val His Thr Ala Lys Thr
385   390   395   400

Gln Pro Arg Glu Gln Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val
                405   410   415

Leu Pro Ile Glu His Gln Asp Trp Leu Thr Gly Lys Glu Phe Lys Cys
                420   425   430

Arg Val Asn His Ile Gly Leu Pro Ser Pro Ile Glu Arg Thr Ile Ser
        435   440   445

99

Lys Ala Arg Gly Gln Ala His Gln Pro Ser Val Tyr Val Leu Pro Pro
    450   455   460

Ser Pro Lys Glu Leu Ser Ser Ser Asp Thr Val Thr Leu Thr Cys Leu
465   470   475   480

Ile Lys Asp Phe Phe Pro Pro Glu Ile Asp Val Glu Trp Gln Ser Asn
            485   490   495

Gly Gln Pro Glu Pro Glu Ser Lys Tyr His Thr Thr Ala Pro Gln Leu
            500   505   510

Asp Glu Asp Gly Ser Tyr Phe Leu Tyr Ser Lys Leu Ser Val Asp Lys
        515   520   525

Ser Arg Trp Gln Gln Gly Asp Thr Phe Thr Cys Ala Val Met His Glu
        530   535   540

Ala Leu Gln Asn His Tyr Thr Asp Leu Ser Leu Ser His Ser Pro Gly
545   550   555   560

Lys

<210> 82
<211> 1686
<212> DNA
<213> Canis familiaris

<400> 82
tcatttaccc ggagaatggg agagggatag atctgtgtag tggttctgta gagcttcatg 60
catcaccgca catgtgaagg tgtctccctg ctgccagcgg ctcttgtcca cagagagctt 120
gctgtacagg aagtaggacc cgtcctcgtc cagctggggc gcagtcgtgt ggtacttgct 180
ctcgggctcc ggctgtccat tgctctgcca ctccacatca atctcaggtg ggaagaagtc 240
tttgatcagg caggtcaggg tgaccgtgtc actggatgac aactcctttg gggatggtgg 300
caggacatac acactgggct gatgggcttg ccctctggct ttggagatag tcctctcgat 360
gggggacggg aggcctatgt ggttgactct gcacttgaac tcctttccgg tgagccagtc 420
ctggtgctca atggggagga cgctgaccac acggtaggtg ctgttgaact gctgctcacg 480
aggctgcgtc ttggctgtgt gcacctcctt accatccacg aaccagctga tctgcacctc 540
agggtcctca cggcccagat ctaacaccac acaggtgatc tcgggtgttc gggtaatcct 600
gaggatgtcc ttgggtttcg ggggaaagat gaagaccgaa ggccctccca gtgattcagg 660
gactgggcat ggggatatac acttgcaggt ggactctttg ggcactggct tgtctacttt 720
agtgttggat ccggtttcct tccagatatc acctttccag cattgttcat cactccactc 780
actccagatt ccatcatctg agcaataaat attcacttta cttcttacca aaaagcataa 840
ttttttggctt tcatttgatg ttcttgtgat ttgtatctca ttctcaactg tggtagtcac 900
ccaagtagta ccatcctctg tgaattcaat ttcataaatg aaacatttgg ctggaatggg 960

100

```
tcctttaggc atgttccatt tcaggttaat ttcctctgaa ttcttcacag taagactaag 1020
gtagtctggt ggcataggtt taactatatt ttgaagctga aaaataaaat agctgggtct 1080
gataggctgg gattctgatg acccattaac acagatgtag aaatctttat agtctgatga 1140
ctccaaatag ggaaacctgc atcccatatt ttttccatta accttgatgt aatcagtaca 1200
ctctgctgaa tggtccaagc cctcatacca gtaaaacaac tggtaattgg tatcaaaatg 1260
gacacccatg ccaggtttcc aagagcagac taaatattgc cagttgtaat atacacagtc 1320
catatcttga attttagttt cccgatttcc ttgtggtgat gtccaataag tagtttctgc 1380
ccatgaactt ctaacttctg atccatttgt gcattgtgct ggcagaagtg tgtttatctt 1440
tgcttcaata cctttgttaa gatcaaaccc atctttgtaa tgtagattct tggtaatgat 1500
ggtcttccag ttttcactat caatgtttcg gtattttaat tcatattcta ttgtgcattc 1560
cttaaaatta tccggaaata atggaggttg ccattgcaaa gagagataac ctaaatatcc 1620
agggtccact atctcaaaat cctgaggagg attaactttt atctcagcat ttgaaagcat 1680
agacat                                                        1686


<210> 83
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:  Synthetic
     Primer

<220>
<223> At locations 9, 18, 21 and 27, n = unknown

<400> 83
athtggacnt ggaayccncc ngarggngc                                   29


<210> 84
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:  Synthetic
     Primer

<220>
<223> At locations 6, 9, 21 and 33, n = unknown

<400> 84
atyttnccng crttrtcytt naccatdaty tgnac                            35


<210> 85
```

101

```
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:  Synthetic
      Primer

<220>
<223> At locations 12, 18 and 21, n = unknown

<400> 85
garathaarg tnaayccncc ncargaytty garat                         35


<210> 86
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:  Synthetic
      Primer

<220>
<223> At locations 12, 22 and 31, n = unknown

<400> 86
tayaargayg gnttctgayy tnaayaargg nathga                        36


<210> 87
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:  Synthetic
      Primer

<220>
<223> At locations 7, 16, 25 and 40, n = unknown

<400> 87
ccaytcnswc cadatnccrt crtcngcrca rtadatrttn acytt              45


<210> 88
```

<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
     Primer

<220>
<223> At locations 9 and 12, n = unknown

<400> 88
gcrtgrtcna rnccytcrta cca   23

<210> 89
<211> 53
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
     Primer

<400> 89
agcggatccc tctatgcttt caaatgctga gataaaagtt aatcctcctc agg   53

<210> 90
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
     Primer

<400> 90
tggacatcac cacaaggaaa tcggg   25

<210> 91
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

Primer

<400> 91
gcacatatgt ctatgctttc aaatgctgaa taaaagttaa tcctcctcag g   51

<210> 92
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
     Primer

<400> 92
aaaggatccg gtttccttcc agatatcatt tccagc   36

<210> 93
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
     Primer

<400> 93
ccgggatcca acactaaagt agacaagcgt g   31

<210> 94
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
     Primer

<400> 94
gcgctcgagt catttacccg gagaatggga ggg   33

<210> 95
<211> 1525
<212> DNA

<213> Canis familiaris

<400> 95

```
gaattcggca cgagggagag gaggagggaa agatagaaag agagagagaa agattgcttg 60
ctacccctga acagtgacct ctctcaagac agtgctttgc tcttcacgta taaggaagga 120
aaacagtaga gattcaattt agtgtctaat gtggaaagga ggacaaagag gtcttgtgat 180
aactgcctgt gataatacat ttcttgagaa accatattat tgagtagagc tttcagcaca 240
ctaaatcctg gagaaatggc ttttgtgcat atcagatgct tgtgtttcat tcttctttgt 300
acaataactg gctattcttt ggagataaaa gttaatcctc ctcaggattt tgaaatattg 360
gatcctggat tacttggtta tctctatttg caatggaaac ctcctgtggt tatagaaaaa 420
tttaagggct gtacactaga atatgagtta aaataccgaa atgttgatag cgacagctgg 480
aagactataa ttactaggaa tctaatttac aaggatgggt ttgatcttaa taaaggcatt 540
gaaggaaaga tacgtacgca tttgtcagag cattgtacaa atggatcaga agtacaaagt 600
ccatggatag aagcttctta tgggatatca gatgaaggaa gtttggaaac taaaattcag 660
gacatgaagt gtatatatta taactggcag tatttggtct gctcttggaa acctggcaag 720
acagtatatt ctgataccaa ctataccatg tttttctggt atgagggctt ggatcatgcc 780
ttacagtgtg ctgattacct ccagcatgat gaaaaaaatg ttggatgcaa actgtccaac 840
ttggactcat cagactataa agattttttt atctgtgtta atggatcttc aaagttggaa 900
cccatcagat ccagctatac agttttttcaa cttcaaaata tagttaaacc attgccacca 960
gaattccttc atattagtgt ggagaattcc attgatatta gaatgaaatg gagcacacct 1020
ggaggaccca ttccaccaag gtgttacact tatgaaattg tgatccgaga agacgatatt 1080
tcctgggagt ctgccacaga caaaaacgat atgaagttga gagggagagc aaatgaaagt 1140
gaagacctat gcttttttgt aagatgtaag gtcaatatat attgtgcaga tgatggaatt 1200
tggagcgaat ggagtgaaga ggaatgttgg gaaggttaca cagggccaga ctcaaagatt 1260
attttcatag taccagtttg tcttttcttt atattccttt gttacttct ttgccttatt 1320
gtggagaagg aagaacctga acccacattg agcctccatg tggatctgaa caaagaagtg 1380
tgtgcttatg aagataccct ctgttaaacc accaatttct tgacatagag ccagccagca 1440
ggagtcatat taaactcaat ttctcttaaa atttcgaata catcttcttg aaaatccaaa 1500
aaaaaaaaaa aaaaaaaaac tcgag                                       1525
```

<210> 96
<211> 1369
<212> DNA
<213> Canis familiaris

<400> 96

```
ggatccgcgc ggatgaaggc tatttgaagt cgccataacc tggtcagaag tgtgcctgtc 60
ggcggggaga gaggcaatat caaggtttta aatctcggag aaatggcttt cgtttgcttg 120
gctatcggat gcttatatac ctttctgata agcacaacat ttggctgtac ttcatcttca 180
gacaccgaga taaaagttaa ccctcctcag gattttgaga tagtggatcc cggatactta 240
ggttatctct atttgcaatg gcaaccccca ctgtctctgg atcattttaa ggaatgcaca 300
gtggaatatg aactaaaata ccgaaacatt ggtagtgaaa catggaagac catcattact 360
aagaatctac attacaaaga tgggtttgat cttaacaagg gcattgaagc gaagatacac 420
acgctttttac catggcaatg cacaaatgga tcagaagttc aaagttcctg ggcagaaact 480
acttattgga tatcaccaca aggaattcca gaaactaaag ttcaggatat ggattgcgta 540
tattacaatt ggcaatattt actctgttct tggaaacctg gcataggtgt acttcttgat 600
accaattaca acttgtttta ctggtatgag ggcttggatc atgcattaca gtgtgttgat 660
```

```
tacatcaagg ctgatggaca aaatatagga tgcagatttc cctatttgga ggcatcagac 720
tataaagatt tctatatttg tgttaatgga tcatcagaga acaagcctat cagatccagt 780
tatttcactt ttcagcttca aaatatagtt aaacctttgc cgccagtcta tcttactttt 840
actcgggaga gttcatgtga aattaagctg aaatggagca tacctttggg acctattcca 900
gcaaggtgtt ttgattatga aattgagatc agagaagatg atactacctt ggtgactgct 960
acagttgaaa atgaaacata caccttgaaa acaacaaatg aaacccgaca attatgcttt 1020
gtagtaagaa gcaaagtgaa tatttattgc tcagatgacg gaatttggag tgagtggagt 1080
gataaacaat gctgggaagg tgaagaccta tcgaagaaaa ctttgctacg tttctggcta 1140
ccatttggtt tcatcttaat attagttata tttgtaaccg gtctgctttt gcgtaagcca 1200
aacacctacc caaaaatgat tccagaattt ttctgtgata catgaagact ttccatatca 1260
agagacatgg tattgactca acagtttcca gtcatggcca aatgttcaat atgagtctca 1320
ataaactgaa tttttcttgc gaaaaaaaaa aaaaaaaatc cgcggatcc       1369


<210> 97
<211> 1525
<212> DNA
<213> Canis familiaris

<400> 97
ctcgagtttt tttttttttt tttttttttgg attttcaaga agatgtattc gaaattttaa 60
gagaaattga gtttaatatg actcctgctg gctggctcta tgtcaagaaa ttggtggttt 120
aacagagggt atcttcataa gcacacactt ctttgttcag atccacatgg aggctcaatg 180
tgggttcagg ttcttccttc tccacaataa ggcaaagaag taacaaaagg aatataaaga 240
aaagacaaac tggtactatg aaaataatct ttgagtctgg ccctgtgtaa ccttcccaac 300
attcctcttc actccattcg ctccaaattc catcatctgc acaatatata ttgaccttac 360
atcttacaaa aaagcatagg tcttcacttt catttgctct cctcttcaac ttcatatcgt 420
ttttgtctgt ggcagactcc caggaaatat cgtcttctcg gatcacaatt tcataagtgt 480
aacaccttgg tggaatgggt cctccaggtg tgctccattt cattctaata tcaatggaat 540
tctccacact aatatgaagg aattctggtg gcaatggttt aactatattt tgaagttgaa 600
aaactgtata gctggatctg atgggttcca actttgaaga tccattaaca cagataaaaa 660
aatctttata gtctgatgag tccaagttgg acagtttgca tccaacattt ttttcatcat 720
gctggaggta atcagcacac tgtaaggcat gatccaagcc ctcataccag aaaaacatgg 780
tatagttggt atcagaatat actgtcttgc caggttccca agagcagacc aaatactgcc 840
agttataata tatacacttc atgtcctgaa ttttagtttc caaacttcct tcatctgata 900
tcccataaga agcttctatc catggacttt gtacttctga tccatttgta caatgctctg 960
acaaatgcgt acgtatcttt ccttcaatgc ctttattaag atcaaaccca tccttgtaaa 1020
ttagattcct agtaattata gtcttccagc tgtcgctatc aacatttcgg tattttaact 1080
catattctag tgtacagccc ttaaattttt ctataaccac aggaggtttc cattgcaaat 1140
agagataacc aagtaatcca ggatccaata tttcaaaatc ctgaggagga ttaactttta 1200
tctccaaaga atagccagtt attgtacaaa gaagaatgaa acacaagcat ctgatatgca 1260
caaaagccat ttctccagga tttagtgtgc tgaaagctct actcaataat atggtttctc 1320
aagaaatgta ttatcacagg cagttatcac aagacctctt tgtcctcctt tccacattag 1380
acactaaatt gaatctctac tgttttcctt ccttatacgt gaagagcaaa gcactgtctt 1440
gagagaggtc actgttcagg ggtagcaagc aatctttctc tctctctttc tatctttccc 1500
tcctcctctc cctcgtgccg aattc                                 1525
```

106

<210> 98
<211> 1369
<212> DNA
<213> Canis familiaris

<400> 98
ggatccgcgg attttttttt tttttttttcg caagaaaaat tcagtttatt gagactcata 60
ttgaacattt ggccatgact ggaaactgtt gagtcaatac catgtctctt gatatggaaa 120
gtcttcatgt atcacagaaa aattctggaa tcattttttgg gtaggtgttt ggcttacgca 180
aaagcagacc ggttacaaat ataactaata ttaagatgaa accaaatggt agccagaaac 240
gtagcaaagt tttcttcgat aggtcttcac cttcccagca ttgtttatca ctccactcac 300
tccaaattcc gtcatctgag caataaatat tcactttgct tcttactaca aagcataatt 360
gtcgggtttc atttgttgtt ttcaaggtgt atgtttcatt ttcaactgta gcagtcacca 420
aggtagtatc atcttctctg atctcaattt cataatcaaa acaccttgct ggaataggtc 480
ccaaaggtat gctccatttc agcttaattt cacatgaact ctcccgagta aaagtaagat 540
agactggcgg caaaggttta actatatttt gaagctgaaa agtgaaataa ctggatctga 600
taggcttgtt ctctgatgat ccattaacac aaatatagaa atctttatag tctgatgcct 660
ccaaataggg aaatctgcat cctatatttt gtccatcagc cttgatgtaa tcaacacact 720
gtaatgcatg atccaagccc tcataccagt aaaacaagtt gtaattggta tcaagaagta 780
cacctatgcc aggtttccaa gaacagagta aatattgcca attgtaatat acgcaatcca 840
tatcctgaac tttagtttct ggaattcctt gtggtgatat ccaataagta gtttctgccc 900
aggaactttg aacttctgat ccatttgtgc attgccatgg taaaagcgtg tgtatcttcg 960
cttcaatgcc cttgttaaga tcaaacccat ctttgtaatg tagattctta gtaatgatgg 1020
tcttccatgt ttcactacca atgtttcggt attttagttc atattccact gtgcattcct 1080
taaaatgatc cagagacagt ggggggttgcc attgcaaata gagataacct aagtatccgg 1140
gatccactat ctcaaaatcc tgaggagggt taactttttat ctcggtgtct gaagatgaag 1200
tacagccaaa tgttgtgctt atcagaaagg tatataagca tccgatagcc aagcaaacga 1260
aagccatttc tccgagattt aaaaccttga tattgcctct ctccccgccg acaggcacac 1320
ttctgaccag gttatggcga cttcaaatag ccttcatccg cgcggatcc   1369

<210> 99
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
     Primer

<400> 99
ctctactatt ggcacagcag cctggga   27

<210> 100
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Primer

<400> 100
agtcagagca aaggaacaac caatgtg   27

<210> 101
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Primer

<400> 101
cctcccgagg gagccagccc g   21

<210> 102
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Primer

<400> 102
cgggctggct ccctcgggag g   21

<210> 103
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Primer

<400> 103
catggtcccc ggcgttcttc c   21

<210> 104
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
     Primer

<400> 104
ggtgagaata ccgacccccac g   21